

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 12, 2003, 00:45:14 ; Search time 189 Seconds
(without alignments)
2675.714 Million cell updates/sec

Title: US-09-515-806A-2
Perfect score: 8544
Sequence: 1 MAGGAGPGRGRDEPPESYP.....KKVSVLFYSDYRILF 1649

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blom62 -TRANS=human40.cdi
-LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:
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2: /cgn2_6/ptodata/2/ina/5B COMB.seq:*
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5: /cgn2_6/ptodata/2/ina/6C COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	480.5	5.6	2729	1	US-07-938-782A-1
2	480.5	5.6	2729	1	US-08-630-524-1
3	480.5	5.6	2729	5	PCT-US93-08131-1
4	416	4.9	2628	1	US-08-143-219-1
5	413.5	4.8	2562	2	US-08-436-771-8
6	413.5	4.8	2562	2	US-08-434-998-8
7	413.5	4.8	2562	2	US-08-487-797-8
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16	284.5	3.3	3332	4	US-09-423-890-11	Sequence 11, Appli
17	282	3.3	3201	2	US-09-211-930-1	Sequence 1, Appli
18	282	3.3	3201	3	US-09-340-993-1	Sequence 1, Appli
19	282	3.3	3201	4	US-09-468-442-1	Sequence 1, Appli
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22	273	3.2	7685	4	US-09-221-017B-1092	Sequence 1092, Ap
23	270	3.2	2028	3	US-09-211-930-12	Sequence 12, Appli
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26	267	3.1	1296	4	US-09-152-406-2	Sequence 2, Appli
27	267	3.1	2322	4	US-09-152-406-1	Sequence 1, Appli
28	267	3.1	2322	4	US-09-152-406-5	Sequence 5, Appli
29	266	3.1	1975	2	US-08-852-743-1	Sequence 1, Appli
30	266	3.1	1975	3	US-09-185-370-1	Sequence 1, Appli
31	265.5	3.1	2390	3	US-08-559-397A-18	Sequence 18, Appli
32	264	3.1	1635	2	US-08-935-760-1	Sequence 1, Appli
33	263.5	3.1	1251	2	US-09-211-930-2	Sequence 2, Appli
34	263.5	3.1	1251	3	US-09-340-993-2	Sequence 2, Appli
35	263.5	3.1	1251	4	US-09-468-442-2	Sequence 2, Appli
36	263.5	3.1	1353	2	US-09-211-930-8	Sequence 8, Appli
37	263.5	3.1	1353	3	US-09-340-993-8	Sequence 8, Appli
38	263.5	3.1	1353	4	US-09-468-442-8	Sequence 8, Appli
39	263	3.1	3435	4	US-09-046-158A-21	Sequence 21, Appli
40	262.5	3.1	4533	4	US-09-171-410-2	Sequence 2, Appli
41	262	3.1	2192	3	US-08-942-001-1	Sequence 1, Appli
42	262	3.1	2192	4	US-09-337-386-1	Sequence 1, Appli
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45	261	3.1	3264	3	US-08-870-529-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-07-938-782A-1
; Sequence 1, Application US/07938782A
; Patent No. 5525513
; GENERAL INFORMATION:
; APPLICANT: Chen, Jane J.
; APPLICANT: London, Irving M.
; TITLE OF INVENTION: DNA Encoding the Heme-Regulated
; NUMBER OF INVENTION: Eukaryotic Initiation Factor 2 alpha kinase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: US
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07938,782A
; FILING DATE: 31-AUG-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: WU101CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)873-8794
; TELEFAX: (404)873-8795
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

LENGTH: 2729 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Rabbit
CELL TYPE: Reticulocytes
FEATURE:
NAME/KEY: misc feature
LOCATION: 113..2149
OTHER INFORMATION: /note= "Expression of HRI
OTHER INFORMATION: mRNA in Human erythroid cells, using as the
OTHER INFORMATION: probe rabbit HRI cDNA from nucleotides 113
OTHER INFORMATION: to 2149."
FEATURE:
NAME/KEY: misc feature
LOCATION: 229..249
OTHER INFORMATION: /note= "Primer used in the
OTHER INFORMATION: amplification of human HRI cDNA sequence
OTHER INFORMATION: using the rabbit HRI cDNA sequence."
FEATURE:
NAME/KEY: misc feature
LOCATION: 543..560
OTHER INFORMATION: /note= "Primer used in the
OTHER INFORMATION: amplification of human HRI cDNA sequence
OTHER INFORMATION: using the rabbit HRI cDNA sequence."
FEATURE:
NAME/KEY: misc feature
LOCATION: 448..468
OTHER INFORMATION: /note= "Primer used in the
OTHER INFORMATION: amplification of human HRI cDNA sequence
OTHER INFORMATION: using the rabbit HRI cDNA sequence."
FEATURE:
NAME/KEY: misc feature
LOCATION: 1009..1031
OTHER INFORMATION: /note= "Primer used in the
OTHER INFORMATION: amplification of a human HRI cDNA sequence
OTHER INFORMATION: using the rabbit HRI cDNA sequence."
PUBLICATION INFORMATION:
AUTHORS: Chen, Jane J.
TITLES: Cloning of the cDNA of the heme-
TITLES: regulated eukaryotic initiation factor
TITLES: 2alpha (elf-2alpha) kinase of rabbit reticulocytes:
TITLES: Homology to yeast GCN2 protein kinase and human
TITLES: double-stranded-RNA-dependent
JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
VOLUME: 88
PAGES: 7729-7733
DATE: September-1991
US-07-938-782A-1
Alignment Scores:
Pred. No.: 1.48e-38 Length: 2729
Score: 480.50 Matches: 184
Percent Similarity: 43.91% Conservative: 97
Best Local Similarity: 28.75% Mismatches: 241
Query Match: 5.62% Indels: 119
DB: 1 Gaps: 29
US-09-515-806A-2 (1-1649) x US-07-938-782A-1 (1-2729)
QY 580 GlnArgGlnPheSerArgTyrPheileGluGluLeuGlnLeuLeuGlyLysGly 599
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QY 600 AlaphedGlyAlaValIleLysValGlnAsnLysLeuAspGlyCysCysTyrAlaValLys 619
DB 650 GGCTATGGCCGAGTGTACAGGTGAGGATTAATAGATGGCCAGTATATGCAATATA 709

QY 620 ArgIleProIleAsnProAlaSerArg---GlnPheArgArgIleLysGlyGluValThr 638
DB 710 AAAATCTCTGATTAAAGGTGCAACTAAACAGATTTGCATGAAGGTATTATTCAGAGAAGTAA 769
QY 639 LeuLeuSerArgIleHisHisGluAsnIleValArgTyrTyrAsnAlaTrrIleGluArg 658
DB 770 GTGCTGGGGCCCTCCAGCACCTCTAATATCGTAGGCTATCACACCGCTGGATAGACAT 829
QY 659 ---HisGluArgProAlaGlyProGlyThrPro-----ProProAspSerGlyProLeu 675
DB 830 GTCCACGTTACGTTTCAAGCAGACAGAGTTCAGTTGCTTCTCTGGAAGTGCCTC 889
QY 676 Ala-----LysAspAspArgAlaAlaArgGlyGlnProAlaSerAspThrAspGlyLeu 693
DB 890 TCTCACCAGGAAGAGACAGAGATCAATATGGTGTAAATAATGATCAAGCAGCAGCTCA 949
QY 694 AspSerValGluAlaAlaAlaProProIleLeuSerSerSerValGluTrpSerThr 713
DB 950 TCCATTATTTTCGCTGAGTTCTCCCAAGAAAAAATCTCTGACGAATGTGCCGTT 1009
QY 714 SerGlyGluArgSerAlaSerAlaArgPheProAla-----ThrGly 727
DB 1010 GAGAGTCAGAAATAACAACTGGTGAATCAACACCACTTAGTGTGAGGACACCGGT 1069
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DB 1208 -----CACACAGAGGTGCGATACCACCTGATGCTGCATATCCAGATGCAGCTGTC 1258
QY 806 GluLysSer-----ThrLeuArgAspThrIleAsp 815
DB 1259 GAGCTGCTCCTGCGGAGTGGATGCCGAGAGAACAGCGCGAGCGAGAGTGGCTGGAC 1318
QY 816 GlnGlyLeu-----TyrArgAspThrValArgLeuTrpArgLeuPheArgGluIleLeu 833
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DB 1379 GAAGGTGTGTTTACATACATAAATGCGCATCGTGCACAGAGACCTGAAGCCTAGAAAT 1438
QY 854 IlePheLeuAspSer-----AspAspHisValIleGlyAspPheGlyLeuAlaThrAsp 872
DB 1439 ATTTTCTTTCATGGTCTCTGATCAACAGAGTAAATAGGAGACTTTGGTCTGGCC-----1492
QY 873 HisLeuAlaPheSerAlaAspSerLysGlnAspAspGlnThrGlyAspLeuIleLysSer 892
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QY 893 AspProSerGlyHisLeuThrGlyMetValGlyThrAlaLeuTyrValSerProGlu--- 911
DB 1541 GAGAGAGACCCACACACACTTCCCGAGTGGGACCTGCTGTCTGTACCTCGCCCGAGCAG 1600
QY 912 ValGlnGlySerThrLysSerAlaTyrAsnGlnLysValAspLeuPheSerLeuGlyIle 931
DB 1601 TTGAAGGA-----TCGGAGTATGATGCCAGTCAGACATGTACAGCCTCGCGCTG 1651
QY 932 IlePhePheGluMetSerTyrHisProMetValThrAlaSerGluArgIlePheValLeu 951
DB 1652 ATCTGTCTGGAGCTC---TTCCAGCCCTTCGGGACAGAGATGGAGCGGCGCAGAGTCTCTG 1708

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Query Match:	5.62%	Indels:	119
DB:	1	Gaps:	29

US-09-515-806A-2 (1-1649) X US-08-630-524-1 (1-2729)

[illegible]

RESULT 3

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; Sequence 1, Application PC/TUS9308131
; GENERAL INFORMATION:
; APPLICANT: Massachusetts Institute Of Technology
; TITLE OF INVENTION: DNA Encoding the Heme-Regulated
; TITLE OF INVENTION: Eukaryotic Initiation Factor 2 alpha Kinase
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kilpatrick & Cody
; STREET: 1100 Peachtree Street

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CITY: Atlanta
STATE: Georgia
COUNTRY: US
ZIP: 30309
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08131
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MIT 5807
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-815-6508
TELEFAX: 404-815-6555
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2729 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HYPOTHETICAL: NO
MOLECULE TYPE: cDNA
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Rabbit
CELL TYPE: Reticulocytes
FEATURE:
NAME/KEY: misc feature
LOCATION: 113..2149
OTHER INFORMATION: /note= "Expression of HRI mRNA in Human erythroid cells,"
FEATURE:
NAME/KEY: misc feature
LOCATION: 229..249
OTHER INFORMATION: /note= "Primer used in the amplification of human HRI cDN
FEATURE:
NAME/KEY: misc feature
LOCATION: 543..560
OTHER INFORMATION: /note= "Primer used in the amplification of human HRI cDN
FEATURE:
NAME/KEY: misc feature
LOCATION: 448..468
OTHER INFORMATION: /note= "Primer used in the amplification of human HRI cDN
FEATURE:
NAME/KEY: misc feature
LOCATION: 1009..1031
OTHER INFORMATION: /note= "Primer used in the amplification of a human HRI c
PUBLICATION INFORMATION:
AUTHORS: Chen, Jane J.
AUTHORS: London, Irving M.
TITLE: Cloning of the cDNA of the heme-regulated
TITLE: eukaryotic initiation factor 2alpha
TITLE: (eIF-2alpha)kinase of rabbit reticulocytes:
TITLE: Homology to yeast GCN2 protein kinase and human
TITLE: double-stranded-RNA-dependent
JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
VOLUME: 88
PAGES: 7729-7733
DATE: September-1991
PCT-US93-08131-1
Alignment Scores:
Pred. No.: 1.48e-38 Length: 2729
Score: 480.50 Matches: 184
Percent Similarity: 43.91%
Best Local Similarity: 28.75%
Query Match: 241 Mismatches: 119
Indels: 119

STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90017

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM compatible
OPERATING SYSTEM: PC-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-08/143,219
FILING DATE: October 25, 1993
CLASSIFICATION: 435

PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/141,244
FILING DATE: October 22, 1993
APPLICATION NUMBER: 07/953,681
FILING DATE: September 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Douglas E. Olson
REGISTRATION NUMBER: 22,798
REFERENCE/DOCKET NUMBER: 204/139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2628 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE: HUMAN PKR GENE, FIGURE 5
INDIVIDUAL ISOLATE:
FEATURE:
NAME/KEY: CDS
LOCATION: 187..1836
US-08-143-219-1

Alignment Scores: Length: 2628
Pred. No.: 5,72e-32 Matches: 179
Score: 416.00 Conservative: 87
Percent Similarity: 37.10% Mismatches: 197
Best Local Similarity: 24.97% Indels: 255
Query Match: 4.87% Gaps: 31
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US-09-515-806A-2 (1-1649) x US-08-143-219-1 (1-2628)

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QY 349 SerLeuValLysSerHisProAsn---ValValArgTyrLeuAlaMetAsnLeuLys 367
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QY 368 GluGlnAspSerIleValValAspLeuValGluHisIleSer-----GlyVal 385
Db 428 CAG-----TTAGTCCTTTA-TTAGTGACAACAAGAATTTCTTCAGAGGATTA 474
QY 386 SerLeuAlaAlaHisLeuSerHisSerGlyProfileProValHisGlnLeuArgTyr 405
Db 475 TCCATGGGGAATTACATAGGCCTTATCAATGAAATTGCC-----CAGAGAAAAGACTA 528
QY 406 ThrAla-----GlnLeuSerGlyLeuAspTyrLeuHisSerValVal 422
Db 529 ACTGTAAATTTATGAACAGTGTGCATCGGG-----GTGCATGGCCAGAGGATTT 579

RESULT 4
US-08-143-219-1
Sequence 1, Application US/08143219
Patent No. 5670330
GENERAL INFORMATION:
APPLICANT: Sonenberg, Nahum
APPLICANT: Katze, Michael G.
APPLICANT: Roy, Sophie
APPLICANT: Koromilas, Antonis E.
APPLICANT: Barber, Glen N.
TITLE OF INVENTION: TUMOR-CELL ASSAY METHOD AND KIT
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon

```

QY 423 His----- 423
Db 580 CATTATAAATGCAAAATGGACAGAAAGATATAGTATTGGTACAGGTTCTACTAAACAG 639
QY 424 -----LysValLeuSerAlaSerAsnVal-----LeuValAspAlaGluGlyThr 438
Db 640 GAAGCAAAACCAATTCGCGCTTAACTTCATATATCTTCAGATATTATCAGAAACAACTCA 699
QY 439 ValLysIleThrAspTyrSerIleSerLysArgLeuAlaAspIleCysLysGluAspVal 458
Db 700 GTGAAA-----TCGACTACTGCTCTCTGCTTCTTGTCTACTAGTGTGAGTCC----- 750
QY 459 PheGluGlnThrArgValArgPheSerAspAsnAlaLeuProTyrLysThrGlyLysLys 478
Db 751 -----CAAAGCAACTTTTAGTGACCAGCACA----- 777
QY 479 GlyAspValTyrArgLeuGlyLeuLeuLeuSerLeuSerGlnGlyGlnGlyCysGly 498
Db 778 -----CTGCTTCTGAATCATCATCTGAAGGT----- 804
QY 499 GluTyrProValThrIleProSerAspLeuProAlaAspPheGlnAspPheLeuLysLys 518
Db 805 -----GACTTCTCAGCAGATACATCAGAGATAATCTAC----- 837
QY 519 CysValCysLeuAspAspLysGluArgTyrSerProGlnGlnLeuLeuLysHisSerPhe 538
Db 838 -----AGTGACAGTTTAAACAGTCTCTGTTGCTTATGAATGGTCTC 879
QY 539 IleAsnProGlnProLysMetProLeuValGluGlnSerProGluAspSerGlyGln 558
Db 880 AGAAATATCAAGGAAGGCAAAA----- 903
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Db 946 ACAAGATATATCTGGCAGCAGAGGTTTGGCATGGATTTAAAGAAATAGAATTAATTTGC 1005
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QY 618 ValLysArgIleProIleAsnProAlaSerArgGlnPheArgIleLysGlyGluVal 637
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Db 1165 -----GATGATTTGAT----- 1176
QY 698 AlaAlaProProIleLeuSerSerValGluTrpSerThrSerGlyGluArg 717
Db 1176 ----- 1176
QY 718 SerAlaSerAlaArgPheProAlaThrGlyProGlySerSerAspAspGluAspAsp 737
Db 1177 -----TATGATCTGACACAGTATGATCT----- 1203
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Db 1216 -----GATTATGATCTCTGAGAACACGAAATAATAGTTCAAG----- 1251
QY 778 AsnGluLysAsnGlyCysHisGluSerGluProSerValThrThrGluAlaValHisTyr 797
Db 1252 -----TCAAGACATAAGTGC----- 1266
QY 798 LeuTyrIleGlnMetGluTyrCysGluLysSerThrLeuArgAspThrIleAsp----- 815
Db 1267 CTTTTCATCAAAATGGAATTTCTGTATAAAGGACCTTGGAAACAATGGATTCAAAAAAGA 1326
QY 816 GlnGlyLeuTyrArgAspThrValArgLeuTyrArgLeuPheArgGluIleLeuAspGly 835
Db 1327 AGAGGCGAGAACTAGACAAAGTTTTTGGCTTTTGGAACTCTTTTGAACAAATAACAAAGGG 1386
QY 836 LeuAlaTyrIleHisGluLysGlyMetIleHisArgAspLeuLysProValAsnIlePhe 855
Db 1387 GTGGATTATATACATTCAAAAAATAATTTATCATAGATCTTAAGCCAAAGTAAATATATTC 1446
QY 856 LeuAspSerAspAspHisValLysIleGlyAspPheGlyLeuAlaThrAspHisLeuAla 875
Db 1447 TTAGTAGATACAAAAACAAGTAAAGATTGGAGACTTTGGACTTTGTAACTCT----- 1497
QY 876 PheSerAlaAspSerLysGlnAspAspGlnThrGlyAspLeuIleLysSerAspProSer 895
Db 1498 -----CTGAAAATGAT----- 1509
QY 896 GlyHisLeuThrGlyMetValGlyThrAlaLeuTyrValSerProGluValGlnGlySer 915
Db 1510 GGAAGCGCAACAAGAGTAAGGAACTTTGGCATACATGAGCCAGAACAGATTCTTCG 1569
QY 916 ThrLysSerAlaTyrAsnGlnLysValAspLeuPheSerLeuGlyIleIlePheGlu 935
Db 1570 -----CAAGACTATGGAAGAGAGTGGACCTCTACGCTTTGGGCTTAATTTCTCTGAA 1623
QY 936 MetSerTyrHisProMetValThrAlaSerGluArgIlePheValLeuAsnGlnLeuArg 955
Db 1624 CTT---CTTCATGATGTGACACTGCTTTTGAACATCAAAAGTTTTCACAGACCTACGG 1680
QY 956 AspProThrSerProLysPheProGluAspPheAspAspGlyGluHisAlaLysGlnLys 975
Db 1681 GATGCGATC-----ATCTCAGATATATTGAT-----AAAAAGAAAAA 1719
QY 976 SerValIleSerTrpLeuAsnHisAspProAlaLysArgProThrAlaThrGluLeu 995
Db 1720 ACTCTTCTACGAAATTAATCTCTCAAGAAACCTGAGGATCGACCTAACACATCTCTGAATA 1779
QY 996 LeuLysSerGluLeuLeuProProGlnMetGluGluSerGluLeuHis 1012
Db 1780 CTAAGGACCTTGACTGTGTGGAAGAAAGCCAGAGAAAAATGAACGACAC 1830

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RESULT 5

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US-08-436-771-8
; Sequence 8, Application US/08436771
; Patent No. 5861300
; GENERAL INFORMATION:
; APPLICANT: Silverman, Robert H.
; APPLICANT: Sengupta, Dibendu N.
; TITLE OF INVENTION: Antiviral Transgenic Plants, Vectors,
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell
; STREET: 200 E. Broward Boulevard
; CITY: Fort Lauderdale
; STATE: Florida
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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QY 856 LeuAspSerAspHisValLysLeuGlyAspPheGlyLeuAlaThrAspHisLeuAla 875
 Db 1450 TTAGTAGATACAAACAGTAAAGATTGGAGACTTTGGACTTAAACATCT----- 1500
 QY 876 PheSerAlaAspSerLysGlnAspGlnThrGlyAspLeuLysSerAspProSer 895
 Db 1501 -----CTGAAATAATGAT----- 1512
 QY 896 GlyHisLeuThrGlyMetValGlyThrAlaLeuTyrValSerProGluValGlnGlySer 915
 Db 1513 GGAAAGCGACACAGGAGTAGGGAACCTTCGGATACATGAGCCGACAGACAGATTTCTTCG 1572
 QY 916 ThrLysSerAlaTyrAsnGlnLysValAspLeuPheSerLeuGlyLysLeuPheGlu 935
 Db 1573 -----CAAGACTATGGAAGGAAGTGGACCTCTACGCTTTGGGCTAATCTTCTCTGAA 1626
 QY 936 MetSerTyrHisProMetValThrAlaSerGluArgIlePheValLeuAsnGlnLeuArg 955
 Db 1627 CTT---CTTCATGTATGTGACACTGCTTTTGAACATCAATCAAGATTTTTCACAGACCTACGG 1683
 QY 956 AspProThrSerProLysPheProGluAspPheAspGlyGluHisAlaLysGlnLys 975
 Db 1684 GATGGCATC-----ATCTCAGATATATTTGAT-----AAAAAGAAAAA 1722
 QY 976 SerValLysSerTrpLeuLeuAsnHisAspProAlaLysArgProThrAlaThrGluLeu 995
 Db 1723 ACTCTTCTCAGAAATTAATCTCAAGAAACCTGAGGATCGACCTTAACACATCTGAAATA 1782
 QY 996 LeuLysSerGluLeuLeuProProGlnMetGluGluSerGluLeuHis 1012
 Db 1783 CTAAGGACCTTGACTGTGTGGGAGAAAGCCAGAGAAATTAAGACGAC 1833

RESULT 6

US-08-434-998-8
 ; Sequence 8, Application US/08434998
 ; Patent No. 5866781
 ; GENERAL INFORMATION:
 ; APPLICANT: Silverman, Robert H.
 ; APPLICANT: Sen Gupta, Dibyendu N.
 ; TITLE OF INVENTION: Anticviral Transgenic Plants, Vectors,
 ; TITLE OF INVENTION: Cells and Methods
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Ruden, Barnett, McClosky, Smith, Schuster &
 ; ADDRESS: Russell
 ; STREET: 200 E. Broward Boulevard
 ; CITY: Fort Lauderdale
 ; STATE: Florida
 ; COUNTRY: USA
 ; ZIP: 33301
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/434,998
 ; FILING DATE:
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/198,973
 ; FILING DATE: 18-FEB-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Manso, Peter J.
 ; REGISTRATION NUMBER: 32,264
 ; REFERENCE/DOCKET NUMBER: CL11363-16
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 305/527/2498
 ; TELEFAX: 305/764/4996
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2562 base pairs

TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cdna
 US-08-434-998-8
 Alignment Scores:
 Pred. No.: 9,85e-32 Length: 2562
 Score: 413.50 Matches: 179
 Percent Similarity: 37.10% Conservative: 87
 Best Local Similarity: 24.97% Mismatches: 198
 Query Match: 4.84% Indels: 254
 DB: 2 Gaps: 31
 US-09-515-806A-2 (1-1649) x US-08-434-998-8 (1-2562)
 QY 329 GluLysGluLysIleAspLysCysLysGlnIleGlnGlyThrGluThrGluPheAsn 348
 Db 344 CAGAGGTGAAGTGAATGAGTCAAGAGGAAGCAAA----- 376
 QY 349 SerLeuValLysLeuSerHisProAsn---ValValArgTyrLeuAlaMetAsnLeuLys 367
 Db 377 -----AAATGCCGACGCCAAATAGCTGTGTGAGTACTTTAATAAGGAAAGGAAGG 427
 QY 368 GluGlnAspSerIleValValAspIleLeuValGluHisIleSer-----GlyVal 385
 Db 428 CAG-----TTAGTCTCTTTA-TTATTGACAAACAAGAAATTTCTTCAGAAAGGATTA 474
 QY 386 SerLeuAlaAlaHisLeuSerHisSerGlyProIleProValHisGlnLeuArgArgTyr 405
 Db 475 TCCATGGGGAATTACATAGGCCCTTATCAATAGAAATTCGCC-----CAGAAAGAAAGACTA 528
 QY 406 ThrAla-----GlnLeuLeuSerGlyLeuAspTyrLeuHisSerAsnSerValVal 422
 Db 529 ACTGTAAATTAATGAACAGTGTGCATCGGG-----CTGCATGGCCAGGAAGATTT 579
 QY 423 His----- 423
 Db 580 CATTATAATGCAAAATGGGACAGAAAGAAATATAGTATTGGTACAGGTTCTACTAAACAG 639
 QY 424 -----LysValLeuSerAlaSerAsnVal-----LeuValAspAlaGluGlyThr 438
 Db 640 GAAGCAAAACAATGGCCGTAAACTTGCATATCTTCAGATATATCAGAAAGAACTCA 699
 QY 439 ValLysIleThrAspTyrSerIleSerLysArgLeuAlaAspIleCysLysGluAspVal 458
 Db 700 GTGAAA---TCTGACTACCTGCTCTCTGTTCTTTTGTCTACTACGTGTGAGTCC----- 750
 QY 459 PheGluGlnThrArgValArgPheSerAspAsnAlaLeuProTyrLysThrGlyLysLys 478
 Db 751 -----CAAAGCAACTCTTTAGTACCAGCACA----- 777
 QY 479 GlyAspValTrpArgLeuGlyLeuLeuLeuSerLeuSerGlnGlyGlnGluCysGly 498
 Db 778 -----CTCGCTTCTGAATCATCTCTGAAGGT----- 804
 QY 499 GluTyrProValThrIleProSerAspLeuProAlaAspPheGlnAspPheLeuLysLys 518
 Db 805 -----GACTTCTCAGCAGATACATCAGAGATA----- 831
 QY 519 CysValCysLeuAspLysGluArgTrpSerProGlnGlnLeuLeuLysHisSerPhe 538
 Db 832 -----AATTCTAACAGTGCACAGTTTAAACAGTCTTCTGTTGCTTATCAATGGTCTC 882
 QY 539 IleAsnProGlnProLysMetProLeuValGluGlnSerProGluAspSerGlyGln 558
 Db 883 AGAATAATCAAGGAGGCAAA----- 906
 QY 559 AspTyrValGluThrValIleProSerAsnArgLeuProSerAlaAlaPheSerGlu 578
 Db 907 -----AGATCTTTGGCCACCCAGATTTGACCTTCTCTGAC-----ATGAAAGAA 948
 QY 579 ThrGlnArgGlnPheSerArgTyrPhe---IleGluPheGluGluGlnLeuLeuGly 597

1627 CTT---CTTCATCTATGTGACACTGCTTTTGAACATCAAAAGTCTTTTCACAGACCTACGG 1683
 956 AspProThrSerProLysPheProGluAspPheAspAspGlyGluHisAlaLysGlnLys 975
 1684 GATGGCATC-----ATCTCAGATATATTGAT-----AAAAAGAAAAA 1722
 976 SerValIleSerTrpLeuLeuAsnHisAspProAlaLysArgProThrAlaThrGluLeu 995
 1723 ACTCTTCTACAGAAATTTACTCTCAAGAAACCTTGAGGATCGACCTAACACATCTGAAATA 1782
 996 LeuLysSerGluLeuLeuProProGlnMetGluGluSerGluLeuHis 1012
 1783 CTAAGGACCTTGACTGTGTGGAAGAAAGCCAGAGAAAAAATGAACGACAC 1833

RESULT 7
 US-08-487-797-8
 ; Sequence 8, Application US/08487797
 ; Patent No. 5866787
 ; GENERAL INFORMATION:
 ; APPLICANT: Silverman, Robert H.
 ; APPLICANT: SenGupta, Dibyendu N.
 ; TITLE OF INVENTION: Transgenic Plants Co-Expressing A
 ; TITLE OF INVENTION: Functional Human 2-5A System
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Holland & Knight
 ; STREET: One E. Broward Boulevard, #1300
 ; CITY: Fort Lauderdale
 ; STATE: Florida
 ; COUNTRY: USA
 ; ZIP: 33301
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/487,797
 ; FILING DATE: 07-JUNE-1995
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Manso, Peter J.
 ; REGISTRATION NUMBER: 32,264
 ; REFERENCE/DOCKET NUMBER: CL11363-16(C)
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 305/468-7811
 ; TELEFAX: 305/463-2030
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2562 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; US-08-487-797-8

Alignment Scores:
 Pred. No.: 9,85e-32 Length: 2562
 Score: 413.50 Matches: 179
 Percent Similarity: 37.10% Conservative: 87
 Best Local Similarity: 24.9% Mismatches: 198
 Query Match: 4.84% Indels: 254
 Gaps: 31
 Db:

US-09-515-806a-2 (1-1649) x US-08-487-797-8 (1-2562)

QY 329 GluLysGluLysIleAspLysCysLysGlnIleGlnGlyThrGluThrGluPheAsn 348
 Db 344 CAGAAGGTGAAGGTAGATCAAGAGGAAGCA----- 376
 QY 349 SerLeuValLysLeuSerHisProAsn---ValValArgTyrLeuAlaMetAsnLeuLys 367
 Db 377 -----AAATGCCGACGCAAAATTAGCTGTGAGATACTTTAATAAGGAAAAAGAGG 427

949 ACAAAGTATACTGTGGCAACAGAGTTTGGCATGATTTTAAAGAAATAGAAATTAATTGGC 1008
 598 LysGlyAlaPheGlyAlaValIleLysValGlnAsnLysLeuAspGlyCysCysTyrAla 617
 1009 TCAGGTGGATTTGGCCAAAGTTTCAAGACAAACACACAGAAATTCAGGAAAGACCTTACGTT 1068
 618 ValLysArgIleProIleAsnProAlaSerArgGlnPheArgArgIleLysGlyGluVal 637
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 638 ThrLeuLeuSerArgLeuHisHisGlnAsnIleValArgTyrTyrAsnAlaTrpIleGlu 657
 1114 AAAGCATTTGGCAAACTTGATCATGTAAATATTTGTTCACTACAATGCGCTGTGG----- 1167
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 1167 ----- 1167
 678 AspAspArgAlaAlaArgGlyGlnProAlaSerAspThrAspGlyLeuAspSerValGlu 697
 1168 -----GATGGATTTGAT----- 1179
 698 AlaAlaProProProIleLeuSerSerValGluTrpSerThrSerGlyGluArg 717
 1179 ----- 1179
 718 SerAlaSerAlaArgPheProAlaThrGlyProGlySerSerAspAspGluAspAsp 737
 1180 -----TATGATCCTGAGACCCAGTGATTTCT----- 1206
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 1207 -----CTTGAGAGCAGT----- 1218
 758 AspIlellePheAspAsnGluAspGluAsnSerLysSerGlnAsnGlnAspGluAspCys 777
 1219 -----GATTATGATCTCGAGACAGCAAGAAATAGTTCAAG----- 1254
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 1255 ---TCAAGACTAAGTGC----- 1269
 798 LeuTyrIleGlnMetGluTyrCysGluLysSerThrLeuArgAspThrIleAsp----- 815
 1270 CTTTTCATCCAAATGGAATCTGTGATAAGGGACCTTGGAAACATGCTGATTAAGAAAGA 1329
 816 GlnGlyLeuTyrArgAspThrValArgLeuTrpArgLeuPheArgGluIleLeuAspGly 835
 1330 AGAGGGAGAACTAGACAAAGTTTGGCTTTGGAACCTTTGGAACAAATAACAAAGGG 1389
 836 LeuAlaTyrIleHisGluLysGlyMetIleHisArgAspLeuLysProValAsnIlePhe 855
 1390 GTGGATTATATACATTCAAAAAAATTAATCATAGAGATCTTAAGCCCAAGTAATATATTC 1449
 856 LeuAspSerAspHisHisValLysIleGlyAspPheGlyLeuAlaThrAspHisLeuAla 875
 1450 TTAGTAGATACAAACAAAGTAAGATTTGGAGACTTTGGACTTTGTAACATCT----- 1500
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 1501 -----CTGAAAAATGAT----- 1512
 896 GlyHisLeuThrGlyMetValGlyThrAlaLeuTyrValSerProGluValGlnGlySer 915
 1513 GGAAGCGAAACAAAGGATAGGGAACCTTGGCATACATGAGCCAGACAGATTTCTTCG 1572
 916 ThrLysSerAlaTyrAsnGlnLysValAspLeuPheSerLeuGlyIlellePhePheGlu 935
 1573 -----CAAGACTATGGAAGGAAGTGGACCTCTAGCTTTGGGCTTAATTTCTGCTGAA 1626
 936 MetSerTyrHisProMetValThrAlaSerGluArgIlePheValLeuAsnGlnLeuArg 955

QY	698	AlaAlaProProProfileLeuSerSerValGluTrpSerThrSerGlyGluArg	717
Db	1179	-----	1179
QY	718	SerAlaSerAlaArgPheProAlaThrGlyProGlySerSerAspAspGluAspAsp	737
Db	1180	-----TATGATCCTGAGACCATGATGATCT-----	1206
QY	738	GluAspGluHisGlyGlyValPheSerGlnSerPheLeuProAlaSerAspSerGluSer	757
Db	1207	-----CTTGAGACGAGT-----	1218
QY	758	AspIleIlePheAspAsnGluAspGluAasnSerLysSerGlnAsnGlnAspGluAspCys	777
Db	1219	-----GATTATGATCTCTGAGACAGCAAAATAGTTCAAG-----	1254
QY	778	AsnGluLysAsnGlyCysHisGluSerGluProSerValThrThrGluAlaValHisTyr	797
Db	1255	---TCAAAGAGCTAAGTGC-----	1269
QY	798	LeuTyrIleGlnMetGluTyrCysGluLysSerThrLeuArgAspThrIleAsp	815
Db	1270	CTTTTCATCCAAATGGAATTCGTGTATAAAGGACCTTGGAACAATGAGTTCGAAAAACA	1329
QY	816	GlnGlyLeuTyrArgAspThrValArgLeuTyrArgLeuPheArgGluIleLeuAspGly	835
Db	1330	AGAGGCGAGAACTAGACAAAGTTTGGCTTTGGAACTCTTTGAAACAATAACAAAGGG	1389
QY	836	LeuAlaTyrIleHisGluLysGlyMetIleHisArgAspLeuLysProValAsnIlePhe	855
Db	1390	GTGGATTATATACATTCAAAAAAATTAATTCATAGATCTTTAAGCCAAAGTAATATTC	1449
QY	856	LeuAspSerAspAspHisValLysIleGlyAspPheGlyLeuAlaThrAspHisLeuAla	875
Db	1450	TTAGTAGATACAAAACAAGTAAGATTGGAGACTTTGGACTTTGAACATCT-----	1500
QY	876	PheSerAlaAspSerLysGlnAspAspGlnThrGlyAspLeuIleLysSerAspProSer	895
Db	1501	-----CTGAAAAATGAT-----	1512
QY	896	GlyHisLeuThrGlyMetValGlyThrAlaLeuTyrValSerProGluValGlnGlySer	915
Db	1513	GGAAAGCGAACAGGAGTAGGGAACTTTGGCATACATGAGCCACAGACATTTCTTCG	1572
QY	916	ThrLysSerAlaTyrAsnGlnLysValAspLeuPheSerLeuGlyIleIlePhePheGlu	935
Db	1573	-----CAAGACTATGGAAGGAGTGGACCTCTACGCTTTGGGCTTAATTTCTGCTGAA	1626
QY	936	MetSerTyrHisProMetValThrAlaSerGluArgIlePheValLeuAsnGlnLeuArg	955
Db	1627	CTT-----CTTCATGATGTGCACACTGCTTTGAAACATCAAAGTTTTTTCACAGACCTACGG	1683
QY	956	AspProThrSerProLysPheProGluAspPheAspAspGlyGluHisAlaLysGlnLys	975
Db	1684	GATGGCATC-----ATCTCAGATATATTTGAT-----AAAAAGAAAAA	1722
QY	976	SerValIleSerTrpLeuLeuAsnHisAspProAlaLysArgProThrAlaThrGluLeu	995
Db	1723	ACTCTTCTACAGAAATTAATCTCTCAAGAGAAACCTCAGGATCGACCTAACACATCTCGAATA	1782
QY	996	LeuLysSerGluLeuLeuProProGlnMetGluSerGluLeuHis	1012
Db	1783	CTAAGGACCTTGACTGTGGAGAAAAAGCCAGAGAAAAATGAACGACAC	1833

RESULT 8

PCT-US95-02058-8

; Sequence 8, Application PC/TUS9502058

; GENERAL INFORMATION:

; APPLICANT: Silverman, Robert H.

; APPLICANT: Sengupta, Dibyendu N.

; TITLE OF INVENTION: Antiviral Transgenic Plants, Vectors,

; TITLE OF INVENTION: Cells and Methods

; NUMBER OF SEQUENCES: 11

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; DATE OF INVENTION:      CELLS AND MET
; NUMBER OF SEQUENCES:    11

```

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
ADDRESSEE: Russell
STREET: 200 E. Broward Boulevard
CITY: Fort Lauderdale
STATE: Florida
COUNTRY: USA
ZIP: 33301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02058
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/198,973

FILING DATE: 18-FEB-1994

ATTORNEY/AGENT INFORMATION:

NAME: Manso, Peter J.

REGISTRATION NUMBER: 32,264

REFERENCE/DOCKET NUMBER: CL11363-16

TELECOMMUNICATION INFORMATION:

TELEPHONE: 305/527/2498

TELEFAX: 305/764/4996

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 2562 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

PCT-US95-02058-8

Alignment Scores:

Pred. No.: 9.85e-32 Length: 2562
Score: 413.50 Matches: 179
Percent Similarity: 37.10% Conservative: 87
Best Local Similarity: 24.97% Mismatches: 254
Query Match: 4.84% Indels: 31
DB: 5 Gaps: 31

US-09-515-806A-2 (1-1649) x PCT-US95-02058-8 (1-2562)

QY 329 GluLysGluLysIleAspLysCysLysGlnGlyThrGluThrGluPheAsn 348
DB 344 CAGAAGGTGAAGGTAGATCAAGAGGAAGCAA----- 376
QY 349 SerLeuValLysLeuSerHisProAsn---ValValArgTyrLeuAlaMetAsnLeuLys 367
DB 377 -----AAATGCCCGCAGCCAAATAGCTGTGAGATCTTAATAAGGAAAGAAAGG 427
QY 368 GluGlnAspAspSerIleValValAspIleLeuValGluHisIleSer-----GlyVal 385
DB 428 CAG-----TTAGTCTTTA-TTATTGACAAACAGAAATCTTCAGAGGAATTA 474
QY 386 SerLeuAlaAlaHisLeuSerHisSerGlyProIleProValHisGlnLeuArgTyr 405
DB 475 TCCATGGGGAATTACATAGGCTTATCAATAGATTGCC-----CAGAGAAAGAAAGCTA 528
QY 406 ThrAla-----GlnLeuLeuSerGlyLeuAspTyrLeuHisSerAsnSerValVal 422
DB 529 ACTGTAAATTTATGAACAGTGTGCATCGGG-----GTGCATGGGCCAGAGGATTT 579
QY 423 His----- 423
DB 580 CATTATAAATGCAAAATGGCAGAAAGAAATATAGTATTGTGTACAGGTTCTACTAAACAG 639
QY 424 -----LysValLeuSerAsnVal-----LeuValAspAlaGluGlyThr 438
DB 640 GAAGCAAAACAAATGGCCGCTAAACTTGCATATCTTCAGATATTATCAGAGAAACCTCA 699

QY 439 ValLysIleThrAspTyrSerIleSerLysArgLeuAlaAspIleCysLysGluAspVal 458
DB 700 GTGAAA---TCTGACTACCTGCTCTGCTGTTCTTTTGTCTACTACGTGTGAGTCC----- 750
QY 459 PheGluGlnThrArgValArgPheSerAspAsnAlaLeuProTyrLysThrGlyLysLys 478
DB 751 -----CAAAGCAACTCTTTTAGTGACCAGCACA----- 777
QY 479 GlyAspValTrpArgLeuGluLeuLeuSerLeuSerGlnGlyGlnGluCysGly 498
DB 778 -----CTCGCTTCTGAATCATCATCTGAAGGT----- 804
QY 499 GluTyrProValThrIleProSerAspLeuProAlaAspPheGlnAspPheLeuLysLys 518
DB 805 -----GACTTCTCAGCAGATACATCAGAGATA----- 831
QY 519 CysValCysLeuAspAspLysGluArgTrpSerProGlnGlnLeuLeuLysHisSerPhe 538
DB 832 -----AATTCTAACAGTGACAGTTTAAACAGCTTCTCGTTGCTTATGAATGCTCTC 882
QY 539 IleAsnProGlnProLysMetProLeuValGluGlnSerProGluAspSerGlyGln 558
DB 883 AGAATAATCAAGAGGAGGCAAAA----- 906
QY 559 AspTyrValGluThrValIleProSerAsnArgLeuProSerAlaAlaPhePheSerGlu 578
DB 907 -----AGATCTTTGGCACCAGATTTGACCTTCCTGCAC-----ATGAAAGAA 948
QY 579 ThrGlnArgGlnPheSerArgTyrPhe---IleGluPheGluGluLeuGlnLeuLys 597
DB 949 ACAAGTATACTGTGGACAGAGGTTTGGCATGGATTTTAAAGAAATAGAAATTAATTGGC 1008
QY 598 LysGlyAlaPheGlyAlaValIleLysValGlnAsnLysLeuAspGlyCysTyrAla 617
DB 1009 TCAGGTGATTTGGCCAAAGTTTCAAAGCAAAACACAGAAATTCGCGAAAGACTTACGTT 1068
QY 618 ValLysArgIleProIleAsnProAlaSerArgGlnPheArgIleLysGlyGluVal 637
DB 1069 ATTAACGCTGTTAAATATAATAAC-----GAGAAGCGGAGCGGTGAAGTA 1113
QY 638 ThrLeuLeuSerArgLeuHisGluAsnIleValArgTyrTyrAsnAlaTrpIleGlu 657
DB 1114 AAAGCATTTGGCAAAACITTCATGTAATAATTTCTCATAATGGCTGTGG----- 1167
QY 658 ArgHisGluArgProAlaGlyProGlyThrProProAspSerGlyProLeuAlaLys 677
DB 1167 ----- 1167
QY 678 AspAspArgAlaAlaArgGlyGlnProAlaSerAspThrAspGlyLeuAspSerValGlu 697
DB 1168 -----GATGATTGTAT----- 1179
QY 698 AlaAlaProProIleLeuSerSerSerValGluTrpSerThrSerGlyGluArg 717
DB 1179 ----- 1179
QY 718 SerAlaSerAlaArgPheProAlaThrGlyProGlySerSerAspGluAspAsp 737
DB 1180 -----TATGATCTGAGACCATGATGATCT----- 1206
QY 738 GluAspGluHisGlyGlyValPheSerGlnSerPheLeuProAlaSerAspSerGluSer 757
DB 1207 -----CTTGAGAGCAGT----- 1218
QY 758 AspIleIlePheAspAsnGluAspGluAsnSerLysSerGlnAsnGluAspGluAspCys 777
DB 1219 -----GATTATGATCTCAGAACACAGCAAAATAGTTCAAGG----- 1254
QY 778 AsnGluLysAsnGlyCysHisGluSerGluProSerValThrGluAlaValHisTyr 797
DB 1255 -----TCAAAGACTAAGTGC----- 1269

QY 798 LeuTyrIleGlnMetGluTyrCysGluLysSerThrLeuArgAspThrIleAsp----- 815
 |||||
 Db 1270 CTTTTCATCCAAATGGAATCTGTGATAAAGGACCTTTGGACATGATGATGAAAGAA 1329
 QY 816 GlnGlyLeuTyrArgAspThrValArgLeuTrpArgLeuPheArgGluLeuLeuAspGly 835
 |||||
 Db 1330 AGAGCGGAGAACTAGACAAAGTTTGGCTTTGGAACTCTTTGAACAAATAACAAAGGG 1389
 QY 836 LeuAlaTyrIleHisGluLysGlyMetIleHisArgAspLeuLysProValAsnIlePhe 855
 |||||
 Db 1390 GTGGATTATATACATTCATAAAATTAATTCATAGAGATCTTAAGCCCAAGTAATATATTC 1449
 QY 856 LeuAspSerAspAspHisValLysIleGlyAspPheGlyLeuAlaThrAspHisLeuAla 875
 |||||
 Db 1450 TTAGTAGATACAAACAAAGTAAGATTGGAGACTTTGGACTTTGAACATCT----- 1500
 QY 876 PheSerAlaAspSerLysGlnAspGlnThrGlyAspLeuIleLysSerAspProSer 895
 |||||
 Db 1501 -----CTGAAATATGAT----- 1512
 QY 896 GlyHisLeuThrGlyMetValGlyThrAlaLeuTyrValSerProGluValGlnGlySer 915
 |||||
 Db 1513 GGAAGGCAACAGGAGTAGGGAACTTTGGATACATGAGCCAGACAGATTTCTTCG 1572
 QY 916 ThrLysSerAlaTyrAsnGlnLysValAspLeuPheSerLeuGlyLeuIlePhePheGlu 935
 |||||
 Db 1573 -----CAAGACTATGAAAGGAGTAGGACTCTACGCTTTGGGGCTAATCTTGTCTGAA 1626
 QY 936 MetSerTyrHisProMetValThrAlaSerGluArgIlePheValLeuAsnGlnLeuArg 955
 |||||
 Db 1627 CTT---CTTCATGATGTGACACTGCTTTTGAACATCAAGTTTTCACAGACCTACCG 1683
 QY 956 AspProThrSerProLysPheProGluAspPheAspAspGlyGluHisAlaLysGlnLys 975
 |||||
 Db 1684 GATGGCATC-----ATCTCAGATATATTTGAT-----AAAGAAAGAA 1722
 QY 976 SerValIleSerTrpLeuLeuAsnHisAspProAlaLysArgProThrAlaThrGluLeu 995
 |||||
 Db 1723 ACTCTTCACAGAAATTTACTCTCAAGAAACCTGAGGATCGACATCAACATCTGAAATA 1782
 QY 996 LeuLysSerGluLeuLeuProProGlnMetGluGluSerGluLeuHis 1012
 |||||
 Db 1783 CTAAGGACCTTGACTGTGTGGAAGAAAGCCAGAGAAATGAACGACAC 1833

RESULT 9

US-09-103-840A-2/c
 ; Sequence 2, Application US/09103840A
 ; Patent No. 6294328
 ; GENERAL INFORMATION:
 ; APPLICANT: FLEISCHMAN, Robert D.
 ; APPLICANT: WHITE, Owen R.
 ; APPLICANT: FRASER, Claire M.
 ; APPLICANT: VENTER, John C.
 ; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
 ; FILE OF INVENTION: TUBERCULOSIS
 ; FILE REFERENCE: 24366-20007.00
 ; CURRENT APPLICATION NUMBER: US/09/103,840A
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 4403765
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium tuberculosis
 ; FEATURE:
 ; OTHER INFORMATION: CDC 1551
 ; OTHER INFORMATION: "n" bases at various positions throughout the sequence
 ; OTHER INFORMATION: represent a, t, c or g
 US-09-103-840A-2

Alignment Scores:
 Pred. No.: 1,81e-14 Length: 4403765
 Score: 303.50 Matches: 204

Percent Similarity: 36.43% Conservative: 149
 Best Local Similarity: 21.05% Mismatches: 378
 Query Match: 3.55% Indels: 240
 DB: 4 Gaps: 42
 US-09-515-806A-2 (1-1649) x US-09-103-840A-2 (1-4403765)
 QY 170 GlnGluGlnArgGluLeuLeuHisGluIleGlnArgArgLysGluGlu-----IleLys 187
 |||||
 Db 19079 CAGCAGCGCGCGCGGTGTACCGCAGGTGCGCGCTAAGCTAACAGAGCTGATGTCGCG 19020
 QY 188 GluGluLysLysArgLysGluMetAlaLysGlnGluArgLeuGluLeuAlaSer---Leu 206
 |||||
 Db 19019 GCCGAGAAAGTCCGACAGCAAGAAAGGCAATCCCGCGGTGCAGATCGCATCCAGAGC 18960
 QY 207 SerAsnGlnAspHisThrSerLysLysAspProGlyGlyHisArgThrAlaAlaIleLeu 226
 |||||
 Db 18959 GGCACCGCGCAACATGGCACC-----GACCTCG-TACACACTCCACCGCGCTTGGTA 18907
 QY 227 His-----GlyGlySerProAspPheValGlyAsnGly 237
 |||||
 Db 18906 CATCGCTTTGCGCCGCAAGCGCCCAAGTGGCTGT-----TGCGCTGCTGCT 18856
 QY 238 LysHisArgAlaAsnSerSerGlyArgSerArgArgGluArgGlnTyrSerValCys--- 256
 |||||
 Db 18855 GGAGAACCGGCTGATCGCTGTCCGCCACCGGAG-----TGCCCT 18814
 QY 257 AsnSerGluAspSerProGlySerCysGluIleLeuTyrPheAsnMetGlySerProAsp 276
 |||||
 Db 18813 CGCGCACCGATCGCGCGCGGTGATCGA-----AGCCGCACTGCAGGGGA 18766
 QY 277 GlnLeuMetValHisLysGlyLysCysIleGlySerAspGluGlnLeuGlyLysLeuVal 296
 |||||
 Db 18765 ACCATGACCCCGAGTTGGCGTGCAGCTGTGCGGCAGATACCGCTGCAGCGCTCATC 18706
 QY 297 TyrAsnAlaLeuGluThrAlaThrGlyGlyPheValLeuLeuLeuTyrGluTyrValLeuGln 316
 |||||
 Db 18705 -----GCCACCGTGTATGGCCCAAGTCTCGGAGCGCGT----- 18670
 QY 317 TrpGlnLysLysMetGlyProPheLeuThrSerGlnGlu---LysGluLysIleAspLys 335
 |||||
 Db 18669 ---GATAACCGGTTGGCGCGGTGTCGCGTGAAGGTGTCAAGAGCGAGTCTCTCTCC 18613
 QY 336 CysLysLysGlnIleGlnGlyThrGluThrGluPheAsnSerLeuValLysLeuSerHis 355
 |||||
 Db 18612 GATCGGAGTTCATCGAACGGTTCGCGCGCGAGCGCCACCGCGATGCTGAACCAT 18553
 QY 356 ProAsnValValArgTyrLeuAlaMetAsnLeuLysGluGlnAsp---AspSerIleVal 374
 |||||
 Db 18552 CCGGCGATCGCCAGCGTGCACACTACGCGCAAGCCAGATGAACGGGAGGTGCGCAG 18493
 QY 375 ValAspIleLeuValGluHisIleSerGlyValSerLeuAlaHisLeuSerHisSer 394
 |||||
 Db 18492 GCCTACTGTGTGAGGTGGTCAACCGCGCGCCCTAAATTCGCTCAAAACGCGACC 18433
 QY 395 GlyProIleProValHisGlnLeuArgTyrThrAlaGlnLeuLeuSerGlyLeuAsp 414
 |||||
 Db 18432 GCGCGGTGCTGTGCGGCGACGCTGGACATCTCGAGCAGACCGCGCGCTCTGCGAG 18373
 QY 415 TyrLeuHisSerAsnSerValValHisLysValSerAlaSerAsnValLeuValAsp 434
 |||||
 Db 18372 ATCGCGATCGCGCTGCTGTGTCACCGCGAGCTCAAAACCGGCAACATCTTGATCACC 18313
 QY 435 AlaGluGlyThrValLysIleThrAspTyrSerIleSerLysArgLeu-----AlaAsp 452
 |||||
 Db 18312 CCCACCGGCGAGTGAAGATCACCGACTTCGCGATCGCCAAAGCGCTCGATGACGAGCC 18253
 QY 453 IleCysLysGluAspValPheGluGlnThrArgValArgPheSer---AspAsnAlaLeu 471
 |||||
 Db 18252 GTGACCCAGACCGCATGGTGTGATGGGCACCGCCCAATATACCGCGCGAGAGCGCTTC 18193
 QY 472 ProTyrLysThrGlyLysLysGlyAspValTrpArgLeuGlyLeuLeuLeuSerLeu 491
 |||||

Db	18192	GCTACAGACGCCGCGCGGACGAGCTATTCTGCGGAGTTGTTGGGTATGAACGC	18133
QY	492	SerGlnGly	
Db	18132	GTTCGGGTAAACGGCGGTTCGCCGCGATGTCCTGACCGTGGCAATGAAGCACATC	18073
QY	498	GlyGluTyrProValThrIleProSerAspLeuProAlaAspPheGlnAspPheLeu-Ly	517
Db	18072	AAGAGCCGCGCGCGCTGCTCCGACCTCCGCGCCCAATGTCCGAGAACTCATCGAG	18013
QY	517	s	
Db	18012	ATAACTCTGTGAAGAACCCCGGATGCTATCGCAGTGGGGACCGTTCGCCGACGCG	17953
QY	527	gTTP	
Db	17952	GTGCAGCGGTGCG	17893
QY	540	nProGlnProLysMetProLeu-ValGluGlnSerProGluAspSerGlyGlnAspT	560
Db	17892	CGGCG	17833
QY	560	YrValGluThrValIleProSer	575
Db	17832	GGCGGACTCGCGCATCCGTCGATCCCGCGCGCGCGCGCGCGCGCGCGCGCG	17774
QY	575	hePheSerGluThrGlnArgGlnPheSerArgTyrPheIleGluPheGluLeuGlnL	595
Db	17773	CGCACGCTTTTCGTCGCG	17743
QY	595	euleuGlyLysGlyAlaPheGlyAlaValIleLysValGlnAsnLysLeuAspGlyCysC	615
Db	17742	CTCTGGCGCGCGCGGTGTCGGGCG	17717
QY	615	ystrAlaValLysArgIleProIleAsnProAlaSerArgGlnPheArgArgIleLysG	635
Db	17717		17717
QY	635	lyGluValThrLeuLeuSerArgLeuHisGluAsnIleValArgTyrAsnAlat	655
Db	17716	GCTGGCANTCATCATCGCGTGTGTCGTCATCAAGCGCC	17675
QY	655	rpIleGluArgHisGluAlaGlyProGlyThrProProProAspSerGlyProL	675
Db	17674	CGGGGACACAGCCGCGACCA	17642
QY	675	eulAlaLysAspArg-AlaAlaArgGlyGln	693
Db	17641	GACCGTGACCAACCCCGGGAACCTCCGCGCAGCAACACTGGCGGACT	17593
QY	694	AspSerValGluAlaAlaProProIleLeuSerSerSerValGluTyrPThr	713
Db	17592	GATGCT	17563
QY	714	SerGlyGlu	716
Db	17562	CGCGGGAAACACGTCATTCTGAGCTGCMAAGCTGGTGTTCGCCGCGACACCGCATTCG	17503
QY	717	ArgSerAlaSerAlaAspPheProAlaThrGly	732
Db	17502	CGCGGTGCTGGCCGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAG	17444
QY	733	AspGluAspAspGluAspGluHisGlyGlyValPheSerGlnSerPheLeuPro	751
Db	17443	CGCTACGAACCTTGGGAAATCCTTGATTTGGGGCATGTCGAGGTCCACTGGCCCGC	17384
QY	752		754
Db	17383	GACCTCCGTTGACCGGACGTTGCGGTCAAGGTGTCGCGGTGATCTAGCCCGCAT	17324
QY	755	SerGluSerAspIlePheAspAsnGluAspGluAsnSerLysSerGlnAsnGlnAsp	774
Db	17323	CCGAGTTTACCTTCGCTTCGCGGTGAGGGCGCAAAACGCGCGCATTAACACACCT	17264

QY	775	Glu	-----AspCysAsnGluLysAsnGlyCysHisGluSerGluProSer	789
Db	17263	GCAATCGTCGCGTCTACGACACCGGTGAA	-----	17234
QY	790	ValThrThrGluAlaValHisTyrLeuTyrIleGlnMetGluTyrCysGluLysSerThr	809	
Db	17233	GCCGAAACGCCCGCGCGCTTTCGCTATCGTATGGAATACATCGACGCGCTTACC	17174	
QY	810	LeuArgAspThrIleAspGlnGlyLeuTyrArgAspThrValArgLeuTyrPArgLeuPhe	829	
Db	17173	CTGCGCGACATTTCCACACCGGCGCGATCGCCCAAGCGCCCATCGAGGTATC	17114	
QY	830	ArgGluIleLeuAspGlyLeuAlaTyrIleHisGluLysGlyMetIleHisArgAspLeu	849	
Db	17113	GCCGACGCTCCCAAGCGCTGAACTTCAGTCATCAGAACGAATCATCCACCGTACGTC	17054	
QY	850	LysProValAsnIlePheLeuAspSerAspAspHisValLysIleGlyAspPheGlyLeu	869	
Db	17053	AAGCGCGCAACATCATGATCAGCGCGCAACATGTCAGTAAAGGTGATGGATTTCGGCATC	16994	
QY	870	AlaThrAspHisLeuAlaPheSerAlaAspSerLysGlnAspAspGlnThrGlyAspLeu	889	
Db	16993	GCCCGC-----GCCATTGCGCAGACGCGCAACAGCGTGACCCAGACC-----	16952	
QY	890	IleLysSerAspProSerGlyHisLeuThrGlyMetValGlyThrAlaLeuTyrValSer	909	
Db	16951	-----GCAGCAGTGATCGGCACGCGCGGCGAGTACCTGTCTATTC	16919	
QY	910	ProGlu-----ValGlnGlySerThrLysSerAlaTyrAsnGlnLysValAspLeuPheSer	928	
Db	16918	CCCGAACAGCGCGGTGATTCGTCGACGCC-----CGATCCGATGTCTATTCC	16868	
QY	929	LeuGlyIleIlePhePheGlu---MetSerTyrHisProMetValThrAlaSerGluArg	947	
Db	16867	TTGGGCTGTGTTCTTTATGAATCTCTACCGGGGAGCCACTTTACCGCGCACTCACCC	16808	
QY	948	IlePheValLeuAsnGln---LeuArgAspProThrSerProLysPheProGluAspPhe	966	
Db	16807	GTCTCGGTGCTACCAACATGTGCGGGAAGACCCGATCCCA-----CCTTCGCGCGCG	16754	
QY	967	AspAspGlyGluHisAlaLysGlnLysSerValIleSerTrpLeuLeuAsnHisAspPro	986	
Db	16753	CACGAAAGCCTCTCCGCGACCTGGACCGCTGCTTCTCAAGGCGCTGGCCAAATCCG	16694	
QY	987	AlaLysArgProThrAlaThrGluLeuLeuLysSerGluLeuLeu-----	1001	
Db	16693	GAACACCGCTATCAGACAGCGCGGAGATGCGCGCGACCTGGTCCGCGTCACACCGT	16634	
QY	1002	ProProProGln-----MetGluGluSerGluLeuHisGluValLeuHisHis	1017	
Db	16633	GAGCGCGCGGAGCGCCCAAGAGTGTACCGATGCGGAGCGGACCTCGCTGTCTGTCT	16574	
QY	1018	ThrLeuThrAsnValAspGly	1024	
Db	16573	GCGCGCGCAACCTTAGCGGT	16553	
RESULT 10				
US-09-103-840A-1/c				
; Sequence 1, Application US/09103840A				
; Patent No. 6294328				
; GENERAL INFORMATION:				
; APPLICANT: FLEISCHMAN, Robert D.				
; APPLICANT: WHITE, Owen R.				
; APPLICANT: FRASER, Claire M.				
; APPLICANT: VENTER, John C.				
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM				
; TITLE OF INVENTION: TUBERCULOSIS				
; FILE REFERENCE: 24366-20007.00				
; CURRENT APPLICATION NUMBER: US/09/103,840A				
; CURRENT FILING DATE: 1998-06-24				
; NUMBER OF SEQ ID NOS: 2				
; SOFTWARE: PatentIn Ver. 1.1				

RESULT 10
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R. M.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.1

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; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Alignment Scores:
Pred. No.: 1.82e-14 Length: 4411529
Score: 303.50 Matches: 204
Percent Similarity: 36.43% Conservative: 149
Best Local Similarity: 21.05% Mismatches: 378
Query Match: 3.55% Indels: 240
DB: 4 Gaps: 42

US-09-515-806A-2 (1-1649) x US-09-103-840A-1 (1-4411529)
QY 170 GlnGluGlnArgGluLeuLeuHisGluLeuGlnArgArgGluGlu-----IleLys 187
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
19079 CAGCAGCGCGCGGGTGTCCCGCAGGTGCGCGCTAAGCTAACAGAGCTGATGTCGC 19020

QY 188 GlnGluLysArgLysGluMetAlaLysGlnGluArgGluLeuAlaSer---Leu 206
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
19019 GCCGAGAAATCCACACAGAGAAAGGGCAATCCCGCGGTGCATCGCATCCCAAGACG 18960

QY 207 SerAsnGlnAspHisThrSerLysLysAspProGlyGlyHisArgThrAlaAlaLeu 226
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
18959 GGCACCGCGCAATCGCAC-----GACCCCTCG-TCACTCCACCGACGCTTGTA 18907

QY 227 His-----GlyGlySerProAspPheValGlyAsnGly 237
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
18906 CATCGCTTTGCGCCCGCACAGCGCCCAAGTGGCTGT-----TGCGGTGCTGT 18856

QY 238 LysHisArgAlaAsnSerSerGlyArgSerArgGluArgGlnTyrSerValCys--- 256
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
18855 GGAGAACGGGGTGTATCGCTGTCGCGCACCGAGG-----TGCCCT 18814

QY 257 AsnSerGluAspSerProGlySerCysGluLeuLeuTyrPheAsnMetGlySerProAsp 276
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
18813 CGCGCACCGCATCGCGCGCGCGGTGATCGA-----AGCCGCACTGCGAGGGGA 18766

QY 277 GlnLeuMetValHisLysGlyLysCysIleGlySerAspGluGlnLeuGlyLysVal 296
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
18765 ACCATGAGCCCCGAGTGGGTGAGCTGACGCTGCGCGCAGATACCGCTGCGACGCCCTATC 18706

QY 297 TyrAsnAlaLeuGluThrAlaThrGlyPheValLeuLeuTyrGluTrpValLeuGln 316
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
18705 -----GCCACCGGTGGTATGGGCCAAGTCTGGAGGCGGTG----- 18670

QY 317 TrpGlnLysLysMetGlyProPheLeuThrSerGlnGlu---LysGluLysIleAspLys 335
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
18669 ---GATAACCGTTGGCGCGCGGTGCGGTGAGGTGCTCAAGACCGAGTTCCTCCTCC 18613

QY 336 CysLysLysGlnIleGlnGlyThrGluThrGluPheAsnSerLeuValLysLeuHis 355
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
18612 GATCGGAGTTTCAGAACCGGTTCGCGCGCAAGCGCGCACCGCGCATGCTGAACCAT 18553

QY 356 ProAsnValValArgTyrLeuAlaMetAsnLeuLysGluGlnAsp---AspSerIleVal 374
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
18552 CCGGCGATCGCCCGTGCAGCTACCGACTACCGGAAAGCGCAGATGAACCGGGAGGTGCGCAG 18493

QY 375 ValAspLeuValGluHisIleSerGlyValSerLeuAlaAlaHisLeuSerHisSer 394
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
18492 GCCTACCTGTGTGGAGCTGGTCAACCGCGAGCCCAATAATCGGTGCTCAACCGCAC 18433

QY 395 GlyProIleProValHisGlnLeuArgArgTyrThrAlaGlnLeuLeuSerGlyLeuAsp 414
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
18432 GCGCGGTGTGTGGCGCAGCGACTGGACATGCTCGACGACACCGCGCGCTCTGCGAG 18373

QY 415 TyrLeuHisSerAsnSerValValHisLysValLeuSerAlaSerAsnValLeuValAsp 434
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
18372 ATCGCGCATCGCGCTGTGTGTCACCGCGAGCTCAACCGCGCAACATCTTGATCACC 18313

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QY 435 AlaGluGlyThrValLysIleThrAspTyrSerIleSerLysArgLeu-----AlaAsp 452
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
18312 CCCACCGCGCAGGTGAAGATCACCGACTTCGGCATCGCAGACCGCTCATCAGCGCCC 18253

QY 453 IleCysLysGluAspValPheGluGlnThrArgValArgPheSer---AspAsnAlaLeu 471
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
18252 GTGACCCAGACCGCATGGTATGGGCACCGCCCAATACATCATCGCCGAGCAGCCCTC 18193

QY 472 ProTyrLysThrGlyLysGlyAspValTrpArgLeuGlyLeuLeuSerLeu 491
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
18192 GGTACAGACCGCAGCCCGCGCAGCGCTTATTCACTGGGAGTTGTTGGGTATGAAGCG 18133

QY 492 SerGlnGly-----GlnGluCys 497
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
18132 GTTTCGGGTAAACCGCGGTTCGCGCGCATGGTGCCTGACCGTGGCAATGAAGCACATC 18073

QY 498 GlyGluTyrProValThrIleProSerAspLeuProAlaAspPheGlnAspPheLeu-Ly 517
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
18072 AAGGAGCCCGCGCGCGCTGCTCCCGACCTGCGCCCAATGTCGAGAACTCATCGAG 18013

QY 517 s-----LysCys---ValCysLeuAspLysGlu-----Ar 527
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
18012 ATAACCTCTGGTGAAGAACCCCGCGATGCGCTATCGAGTGGGGACCGTTTCGCGACGCG 17953

QY 527 gTTP-----SerProGlnGlnLeuLeuLysHisSerPheIleAs 540
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17952 GTGGCAGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 17893

QY 540 nProGlnProLysMetProLeu-ValGluGlnSerProGluAspSerGlyGlyGlnAspT 560
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17892 CGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 17833

QY 560 yrValGluThrValIleProSer-----AsnArgLeuProSerAlaAlap 575
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17832 GCGCGGACTGCGCGCATCCGTCGATCCGCGCGCACCGGTGGTCAACCGCGCGCGCGCG 17774

QY 575 hePheSerGluThrGlnArgGlnPheSerArgTyrPheIleGluPheGluGlnLeuGlnL 595
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17773 -----GCGCACGTTTTCGTCCGG---TCAGCGTGGCGCTG 17743

QY 595 euLeuGlyLysGlyAlaPheGlyAlaValIleLysValGlnAsnLysLeuAspGlyCysC 615
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17742 CTCTGGCGCGCGCGGTGCTGGCGG---TCAGCGTGGCGCTG 17717

QY 615 ysTyrAlaValLysArgIleProIleAsnProAlaSerArgGlnPheArgIleLysG 635
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17717 ----- 17717

QY 635 lyGluValThrLeuLeuSerArgLeuHisGluAsnIleValArgTyrTyrAsnAlaT 655
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17716 -----GCTGGCAATCATCGCGCTGCTGCTCATCAAGCGCGC- 17675

QY 655 rPleGluArgHisGluArgProAlaGlyProGlyThrProProAspSerGlyProL 675
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17674 -----CGGGACCAACAGCGCGCGCA-----GGCAGCGCGCGC- 17642

QY 675 euAlaLysAspAspArg-AlaAlaArgGlyGln---ProAlaSerAspThrAspGlyLeu 693
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17641 -----GACCGTGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 17593

QY 694 AspSerValGluAlaAlaProProIleLeuSerSerValGluTrpSerThr 713
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17592 GATGCT-----AGCCCGCGACTCAATGGACGGA 17563

QY 714 SerGlyGlu----- 716
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17562 CCGCGGGAACAGCTTCTGGACTGCAAGCTGGTGTTCGCGCGCGCACCGCGCATTCG 17503

QY 717 ArgSerAlaSerAlaArgPheProAlaThrGly-----ProGlySerSerAsp 732
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17502 CGCGCGTCTGCTGCGCGCGATACGAGATACCGCAATGACACCGCTTCCAC-CTGTCGAC 17444

QY 733 AspGluAspAspGluAspGluHisGlyValPheSerGlnSerPheLeuPro--- 751

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us-09-515-806a-2.rni

Thu Jun 12 14:34:04 2003

TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING CELL
RESPONSIVENESS TO EXTERNAL SIGNALS

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lahive and Cockfield

STREET: 60 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/472,934

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/440,421

FILING DATE: 15-May-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/354,516

FILING DATE: 21-FEB-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 5,405,941

FILING DATE: 15-Apr-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/323,460

FILING DATE: 14-Oct-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/11690

FILING DATE: 14-Oct-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/04178

FILING DATE: 15-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Giulio A. DeConti, Jr. Esq.

REGISTRATION NUMBER: 31,503

REFERENCE/DOCKET NUMBER: CPI-004DVCP2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 3089 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 400..2280

US-08-472-934-5

Alignment Scores:

Pred. No.:	Length:	3089
Score:	238e-18	125
Percent Similarity:	284.50	86
Best Local Similarity:	39.89%	211
Query Match:	23.63%	107
DB:	3.33%	20

US-09-515-806A-2 (1-1649) x US-08-472-934-5 (1-3089)

QY	77	VallysCysProThrTyrProAspValValProGluLeuGlu	-----LeuLys 93
Db	800	CTGGAGTGTCCAGGCAGGTTCGGATCAAGCCTTCCCGATCTGCGGGGATATAATACCA	859
QY	94	AsnAlaLysGlyLeuSerAsnGluSerValAsnLeuLysSerArgLeuGluLeu	113
Db	860	TCTACCAAGTCTCTGAGCCCAAGACGACCTGTCTGTCA	-----901

RESULT 11

US-08-472-934-5

; Sequence 5, Application US/08472934

; Patent No. 5753446

; GENERAL INFORMATION:

; APPLICANT: JOHNSON, GARY L.

QY 114 AlaLysLysHisCysGlyGluValMetIlePheGluLeuAlaTyrHisValGlnSerPhe 133
 DB 902 GTCCAGAACCCCTGGCGAAGCTCTCTCCCGCG-----GATATGTAC 946
 QY 134 LeuSerGluHisAsnLysProProLysSer-PheHisGluGluMetLeuGluArgAr 153
 DB 947 CTGAGCGAACACAGCATTTCCCGCAAGATCTCTATACGACATCAACAGGAAAGTG 1006
 QY 153 GAlaGlnGluGlnGlnArgLeuLeuGluAlaLys-----ArgLysG1 168
 DB 1007 AATTCAATCCAGACACAGGACAGAGTGTATGTAGATCCCTCAGACGTGCGGAAAT 1066
 QY 168 uLugLndGlnArgLuleLeuHisGlnGlnArgArg-LysGluGluLileLysG 188
 DB 1067 CTTGTGTGAGGAAGCTGCAATCTCTGACAGGTGACGACAGCCCATCTTCAGAAAT 1126
 QY 188 luGluLysLysArgLysGluMetAlaLysGlnGlnArgLeuGluLeuAlaSerLys 208
 DB 1127 CACAAATGTCGAGCCCGAGCTTCCACAGAACAGAAAGATGCTCAGATCGGAGA 1186
 QY 208 snGlnAspHisThrSerLysLysAspProGlyGly-----HisArgThrAlaAla 225
 DB 1187 CCCAGCTCTAT---GATAAGGTGTCAAAGGTGGAACCTATCCAGGCGCTACATGRT 1243
 QY 225 leLeuHisGlyGlySerProAspPheValGlyAsnGlyLysHisArgAlaAsnSerS 245
 DB 1244 CTGTGAT-----CACAAAGACTACAATGATG 1270
 QY 245 lyArgSerArg-----AtgGluArgGlnTyrSerValCysAsnSerGluAspS 261
 DB 1271 GCAGAGAACAATTTCCCGAATACAGCGCATCAAGCAACCTATTCCTCTGTGTCCT 1330
 QY 261 erProGlySerCysGluLileLeuTyrPheAsnMetGlySerProAspGlnLeuMetVal 281
 DB 1331 CAACTCGCTCTGTGACCAAAATGCGAGAAATGGGTGAGTGTGCAATCTGAC 1390
 QY 281 isLysGlyLysCysLileGlySerAspGluGln----- 291
 DB 1391 CCGGTGGCGCTACGGAGTGAGACAGTGAATGCCCTCACTGTGAGGAAGGAATG 1450
 QY 292 -----LeuGlyLysLeuValTyrAsnA 299
 DB 1451 TGCCAAACCAAAATCTCTAGTGTCCATCAATTTGGCGTGGGGAAGCTCTG 1503
 QY 299 laLeuGluThrAlaThrGlyGlyPheValLeuLeuTyrGluTyrValLeuGlnTrpGln 319
 DB 1504 -----GGTCAAGGTGCTTGGCAGGGGTCTAC-----TTGTGCTATGATG 1543
 QY 319 ysLysMetGlyProPheLeuThrSerGlnGluLysGlu-----LysLileAspLysC 336
 DB 1544 TGGACACAGGACGTGAATCTCTTAAGCAGGTCCAGTTTGACCCAGATAGTCTTGAGA 1603
 QY 336 ysLysLysGlnleGlnGlyThrGluThrGluPheAsnSerLeuValLysLeuSerHisP 356
 DB 1604 CAAGCAAGGAGTGAGTGTCTTGAGTGTGAGATCCAGTTGTCTGAAGAACCCTGCAGCATG 1663
 QY 356 roAsnValValArgTyrLeuAlaMetAsnLeuLysGluGlnAspAspSerlileValVal 376
 DB 1664 AGCGCATTTGCACTACTACGGTGC---CTGGCGGACCGTGTGAAGAATCTCTCAAC 1719
 QY 376 spLileLeuValGluHisLileSerGlyValSerLeuAlaAlaHisLeuSerHisSerGlyP 396
 DB 1720 --ATCTTTATGGAGTATATCCAGGGGGCTCTGTAAAGACACCATTTGAAGGCTACGGAG 1777
 QY 396 rolleProValHisGlnLeuArgTyrThrAlaGlnLeuLeuSerGlyLeuAspTyrL 416
 DB 1778 CTCTGACAGAGGTGTGACCCGCAAGTACCCGCGAGATTCTGAGGGCATGTCTATACC 1837
 QY 416 eutHisAsnSerValValHisLysLysValLeuSerAlaSerAsnValLeuValAspAlaG 436
 DB 1838 TGCACAGCAACATGATTGTGCTCGGGACATCAAGGAGCCATATCTCTCCGAGACTCAG 1897

QY 436 luGlyThrValLysIleThrAspTyrSerIleSerLysArgLeuAlaAspLileCysLysG 456
 DB 1998 CTGGGAATGTGAAGCTTTGGGGCCAGCAACGCTTACAGACCATCTGC----- 1953
 QY 456 luAspValPheGluGlnThrArgValArgPheSerAspAsnAlaLeuProTyr----- 473
 DB 1954 -----ATGTCAAGGACAGGCAATTCGC---TCTGTCACTGGCACACCTTACTGGATGA 2002
 QY 474 -----LysThrGlyLysLysGlyAspValTrpArgLeuGlyL 486
 DB 2003 GTCTCAAGTCATCAGTCGCGAGGCTATGGAAGAAAGGACAGCTGTGGAGCCTGGCT 2062
 QY 486 euLeuLeuLeuSer-----LeuSerGlnGlyGlnGlnCysGlyGlnTyrProVal----- 502
 DB 2063 GTACTGTGTGGAATGCTGACAGAGAACACACCTTGGGCAGAGTATGAAGCTATGGCTG 2122
 QY 503 -----ThreProSerAspLeuProAlaA 511
 DB 2123 CCAATTTCAAGATGCCCCAGCCTACCAATCTCTCAGCTGCCCTTCCATCTCAGAAC 2182
 QY 511 spPheGlnAspPheLeuLysLysCysValCysLeuAspAspLysGluArgTrpSerProG 531
 DB 2183 ACGGCAAGGACTTCTGTAGGCGC---ATATTGTGGAAGCTCTGTCAGAGACCTCAGCTG 2239
 QY 531 lnGlnLeuLeuLysHisSerPhe 538
 DB 2240 AGGAGCTGCTCACACACACTTT 2262

RESULT 12
 US-08-323-460A-5
 ; Sequence 5, Application US/08323460A
 ; Patent No, 5854043
 ; GENERAL INFORMATION:
 ; APPLICANT: JOHNSON, GARY L.
 ; TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING CELL
 ; OF INVENTION: RESPONSIVENESS TO EXTERNAL SIGNALS
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SHERIDAN ROSS & MCINTOSH
 ; STREET: 1700 LINCOLN STREET, SUITE 3500
 ; CITY: DENVER
 ; STATE: CO
 ; COUNTRY: USA
 ; ZIP: 80203
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: 14-OCT-1994
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/049,254
 ; FILING DATE: 14-APR-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KOVARIK, JOSEPH E.
 ; REGISTRATION NUMBER: 33,005
 ; REFERENCE/DOCKET NUMBER: 2879-1-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 303/863-9700
 ; TELEFAX: 303/863-0223
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3089 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 400...2280

Thu Jun 12 14:34:04 2003

US-08-323-460A-5

Alignment Scores:

Pred. No.: 2,38e-18 Length: 3089
Score: 284.50 Matches: 125
Percent Similarity: 39.8% Conservatives: 86
Best Local Similarity: 23.63% Mismatches: 211
Query Match: 3.33% Indels: 107
DB: 2 Gaps: 20

US-09-515-806A-2 (1-1649) x US-08-323-460A-5 (1-3089)

QY 77 valLysCysProProthThyProaspValValProGluLleGlu-----LeuLys 93
DB 800 CTGGAGTTCAGGAGGTTCGGATCAAGCCTTCCTCCAGTCTCGAGGGGATATAATACCA 859
QY 94 AsnAlaLysGlyLeuSerAsnGluSerValAsnLeuLeuLysSerArgLeuGluLeu 113
DB 860 TCTACCAAGCTCTGAGCCCAAGCAGCAGCCCTCTCTGTCA----- 901
QY 114 AlaLysLysHisCysGlyGluValMetIlePheGluLeuAlaTyHisValGlnSerPhe 133
DB 902 GCTCCCAAGAACCTGGCCGAGCTCTCTCCCTCCCGG-----GATATGTAC 946
QY 134 LeuSerGluHisAsnLysProProLysSerPheHisGluGluMetLeuGluAtgAr 153
DB 947 CTGAGCGACAACAGCAGCATTTGCCCGGCAAGGATCTTATACGAGCATCAACAGCGAGGTG 1006
QY 153 gAlaGlnGluGluGlnArgLeuLeuGluAlaLys-----ArgLysG 168
DB 1007 AATTATCTCCAGAGCAGCAGGAGCATGATGTATGTATCCCTCAGCAGTGGCGGAAAT 1066
QY 168 uGluGlnGluGlnArgGluLeuHisGlnArgArgLysGluGluLleLysG 188
DB 1067 CTTGTCCAGGAGTGCATCTCTTGACAGGTGACGAGCAGCAGCCATCTTCAGGAAT 1126
QY 188 luGluLysArgGluMetAlaLysGlnGluArgLeuGluLleAlaSerLeuSerA 208
DB 1127 CACAAATGTCCTCCGAGCCGAGGTCTCCAGACAACAGAAAGATCTCAGATCGGAGA 1186
QY 208 enGlnAspHisSerLysLysAspProGlyGly-----HisArgThrAlaAlaI 225
DB 1187 CCCAGCTCTAT---GATAAAGGTGCAAGGTGCAAGCTATCCCGCGCTACCATGTGT 1243
QY 225 leuHisGlyCysSerProaspPheValGlyAsnGlyLysHisArgAlaAsnSerSerG 245
DB 1244 CTGTGCAT-----CACAAAGACTACAATGATG 1270
QY 245 lyArgSerArg-----ArgGluArgGlnTySerValCysAsnSerGluAspS 261
DB 1271 GCAGAAGAACATTTCCCGAATACGAGCGCATCAAGCAACCTATTCACTCTGTGCGCCT 1330
QY 261 erProGlySerCysGluLleLeuTyPheAsnMetGlySerProaspGlnLeuMetValH 281
DB 1331 CAAGTCCTCTTGAGCAAAATGCGGAGAACTGGGTGTAGCTGTGCAATACCTGGACC 1390
QY 281 isLysGlyLysCysLleGlySerAspGluGln----- 291
DB 1391 CCCGTGGCGCCTACGGAGTGAGCAGTGTGAGATGCCCTCACTGTGCGAGAAAGGAATG 1450
QY 292 -----LeuGlyLysLeuValTyRAsnA 299
DB 1451 TGCCAACCAAAATCTCTAGTGTCTCCATCAATTTGGCGTGGGGGAGCTCTCTG 1503
QY 299 laLeuGluThrAlaThrGlyGlyPheValLeuLeuTyRTrpValLeuGlnTrpGlnL 319
DB 1504 -----GTCAGAGTGGCTTCGGCAGGCTCTAC-----TTGTGTATATG 1543
QY 319 ysLysMetGlyProPheLeuThrSerGlnGlyLysGlu-----lysLleAspLysC 336
DB 1544 TGGACACAGACGTCGTAACCTTCTTCAAGCAGGTCCAGTTTGACCCAGATAGTCTCTGAGA 1603
QY 336 ysLysLysGlnLleGlnGlyThrGluThrGluPheAsnSerLeuValLysLeuSerHisP 356

DB 1604 CAAGCAAGGAGGTGAGTGTCTCTGGAGTGTGAGATCCAGTTGTGAAGAACCTTCAGCATG 1663
QY 356 roAsnValValArgTyRLeuAlaMetAsnLeuLysGluGlnAspSerIleValValA 376
DB 1664 AGCGCATTTGTGCACTACTACGGGTGC---CTGGGAGCGCTGCTGAGAAGATCTCTCACC- 1719
QY 376 spLleLeuValGluHisIleSerGlyValSerLeuAlaHisLeuSerHisSerGlyP 396
DB 1720 --ATCTTTTATGAGTATATCCAGGGGGCTCTGTAAAGACCAAGTGTGAAGGGCTACGGAG 1777
QY 396 rolleProValHisGlnLeuArgTyRThrAlaGlnLeuLeuSerGlyLeuAspTyR 416
DB 1778 CTCTGACAGAGGTGTACCCGCAAGTACACCCGCGAGATTTCTGGAGGCGATGTCTATACC 1837
QY 416 euHisSerAsnSerValValHisLysValLeuSerAlaSerAsnValLeuValAspAlaG 436
DB 1838 TGCACAGCAACATGATTTGTGATCGGACATCAAGGGAGCCAATATCTCTCCGAGACTCAG 1897
QY 436 luGlyThrValLysIleThrAspTyRSerIleSerLysArgLeuAlaAspIleCysLysG 456
DB 1898 CTGGGAATGTGAAGCTTGGGGATTTGGGGCCAGCAAAACCCCTACAGCATCTGC--- 1953
QY 456 luAspValPheGluGlnThrArgValArgPheSerAspAsnAlaLeuProTyR----- 473
DB 1954 -----ATGTACAGGACAGCATTCGC---TCTGTCACTGGCAGCACCCTACTGGATGA 2002
QY 474 -----LysThrGlyLysLysGlyAspValTrpArgLeuGlyL 486
DB 2003 GTTCCTGAAGTATCATGTGGCGAGGCTATGGAAGAAAGGACAGCTGTGGAGCCTGGGCT 2062
QY 486 euLeuLeuLeuSer---LeuSerGlnGlyGlnGluCysGlyGlyTyRProVal----- 502
DB 2063 GTACTGTGTGGAATGTCTGACAGAGAAACACCTTGGGAGAGTATGAAGCTATGGCTG 2122
QY 503 -----ThrIleProSerAspLeuProAlaA 511
DB 2123 CCATTTTCAAGATTGCCAGCCAGCTACCAATCTCTCAGTGCCTCTCCATCTCAGAAC 2182
QY 511 spPheGlnAspPheLeuLysLysCysValCysLeuAspAspLysGluArgTrpSerProG 531
DB 2183 ACGGAGGAGTCTCTCTGAGGCGC---ATATTTGTGGAAGCTCTGTCAGAGACCTCAGCTG 2239
QY 531 lngLlnLeuLysHisSerPhe 538
DB 2240 AGGAGTGTCTCACACACCATTTT 2262

RESULT 13

US-08-461-146C-5
Sequence 5, Application US/08461146C
Patent No. 5981265
GENERAL INFORMATION:
APPLICANT: JOHNSON, GARY L.
TITLE OF INVENTION: METHODS FOR REGULATING MEKK PROTEIN ACTIVITY
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive and Cockfield
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,146C
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/354,516

FILING DATE: 21-FEB-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/049,254
 FILING DATE: 15-APR-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/323,460
 FILING DATE: 14-OCT-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/11690
 FILING DATE: 14-OCT-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/04178
 FILING DATE: 15-APR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: KARA, Catherine J.
 REGISTRATION NUMBER: P41,106
 REFERENCE/DOCKET NUMBER: CPI-004CN3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 227-5941
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3089 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 400..2280
 US-08-461-146C-5

Alignment Scores:

Pred. No.: 2,38e-18 Length: 3089
 Score: 284.50 Matches: 125
 Percent Similarity: 39.89% Conservative: 86
 Best Local Similarity: 23.63% Mismatches: 211
 Query Match: 3.33% Indels: 107
 DB: 2 Gaps: 20

US-09-515-806A-2 (1-1649) x US-08-461-146C-5 (1-3089)

QY 77 ValLysCysProThrTyProAspValValProGluLeuLysGlu-----LeuLys 93
 Db 800 CTGGAGTCTCCAGCAGGTCGGATCAAGCTTCCAGTCTCCAGTCTGAGGGGATATAATACCA 859
 QY 94 AsnAlaLysGlyLeuSerAsnGluSerValAsnLeuLysSerArgLeuGluLys 113
 Db 860 TCTACCAAGCTCTTGAGCCCGAGGAGGAGGACCTGTCTGTCA-----901
 QY 114 AlaLysLysHisCysGlyGluValMetIlePheGluLeuAlaTyRHisValGlnSerPhe 133
 Db 902 GCTCCAGAACCTTGGCCGAGGCTCTCTCCCTCCCGG-----GATATGTAC 946
 QY 134 LeuSerGluHisAsnLysProProLysSerPheHisGluGluMetLeuGluArgAr 153
 Db 947 CTGAGCAGCAACAGCAATTCGCCGCAAGGATCTTATCAGAGCATCAACAGCGAGGTG 1006
 QY 153 GAlaGlnGluGlnGlnArgLeuLeuGluAlaLys-----ArgLysG1 168
 Db 1007 AATTATCCAGAGCAGGACGACAGTGTATGCTAGATCCCTCAGCAGTCCGCAAAAT 1066
 QY 168 uGluGlnGluArgGluLeuHisGluLeuGlnArgArgArg-LysGluGluLeuLysG 188
 Db 1067 CCTTGTGAGAGCTCCCAATCTTGGACAGTCCAGCAGCAGCCATCTTTCAGGAAT 1126
 QY 188 luGluLysArgLysGluMetAlaLysGlnGluArgLeuGluLeuAlaSerLeuSerA 208
 Db 1127 CACAAATGTCGCGAGCCGAGCTCCAGACACAGAAAGAAATGTCTCAGATCGGAGA 1186
 QY 208 snGlnAspHisThrSerLysLysAspProGlyGly-----HisArgThrAlaAlaI 225
 Db 1187 CCCAGCTCTAT---GATAAAGGTGTCAAAGGTGGAACCTATCCAGCGGCTTACCATGTGT 1243

QY 225 leLeuHisGlyGlySerProAspPheValGlyAsnGlyLysHisArgAlaAsnSerSerG 245
 Db 1244 CTGTGCAT-----CACAAAGACTACAATGATG 1270
 QY 245 lyArgSerArg-----AtgGluArgGlnTySerValCysAsnSerGluAsps 261
 Db 1271 GCAGAAAGAACATTTCCCGCAATACAGCGCATCAAGCAACCTATTCACTCTGTGGTGCCT 1330
 QY 261 erProGlySerCysGluLeuLeuTyRpheAsnMetGlySerProAspGlnLeuMetValH 281
 Db 1331 CAAGTCGCTCTGTAGCACAATAATGGCGAACAATGGGTGTAGCTGTGCAATACCTGGACC 1390
 QY 281 isLysGlyLysCysylleGlySerAspGluGln-----291
 Db 1391 CCGTGGGCGCTACGGAGTGCAGACAGTAGAGATGCCCTCACTGTGTGAGGAAAGGAATG 1450
 QY 292 -----LeuGlyLysLeuValTyRAsnA 299
 Db 1451 TGCCAAACCAATCTCTAGTGTCTCCATCAATTGGCGTCGGGGAAGCTCTCTG-----1503
 QY 299 laLeuGluThrAlaThrGlyPheValLeuLeuTyRglnTrpGlnL 319
 Db 1504 -----GGTCAAGTGCCTTCGGCAGGGTCTAC-----TTGTCTATGATG 1543
 QY 319 ysLysMetGlyProPheLeuThrSerGlnGluLysGlu-----LysIleAspLysC 336
 Db 1544 TGGACACAGAGCGTGAACCTTCTTAAGCAGGTCCAGTTTGACCCAGATAGTCCTGAGA 1603
 QY 336 ysLysLysGlnIleGlnGlyThrGluThrPheAsnSerLeuValLysLeuSerHisP 356
 Db 1604 CAAGCAAGGAGGTGAGTGTCTGGAGTGTGAGATCCAGTTGCTGAAGAACTCCAGCATG 1663
 QY 356 roAsnValValArgTyRLeuAlaMetAsnLysGluGlnAspAspSerIleValValA 376
 Db 1664 AGCGCATTTGTCAGTACTACGGTGC---CTGGGAGCGGTCTGTGAGAGATCTCTCACC- 1719
 QY 376 spIleLeuValGluHisIleSerGlyValSerLeuAlaHisLeuSerHisSerGlyP 396
 Db 1720 --ATCTTTATGGAGTATATGCCAGGGGCTCTGTAAGACACCATTTGAAGGCTACGGAG 1777
 QY 396 rolleProValHisGlnLeuArgAtgTyRThrAlaGlnLeuLeuSerGlyLeuAspTyR 416
 Db 1778 CTCTGACAGAGAGTGTGACCCGCAAGTACCCCGGAGATTCTGGAGGCGATGTCTATACC 1837
 QY 416 euHisSerAsnSerValValHisLysValSerAlaSerAsnValLeuValAspAlaG 436
 Db 1838 TGACAGCAACATGATTTGTGCATCGGACATCAAGGAGGCCAATATCTCCGAGACTCAG 1897
 QY 436 luGlyThrVallyslleThrAspTyRSerIleSerLysArgLeuAlaAspIleCysLysG 456
 Db 1898 CTGGGAATGTGAAGCTTGGGGATTTGGGGCCAGCAAAACGCTACAGACCATCTGC---1953
 QY 456 luAspValPheGluGlnThrArgValArgPheSerAspAsnAlaLeuProTyR-----473
 Db 1954 -----ATGTGAGGAGCAGGCATTCG---TCTGTCACTGGCACACCTTACTTGGATGA 2002
 QY 474 -----LysThrGlyLysLysGlyAspValTrpArgLeuGlyL 486
 Db 2003 GTCTTGAAGTCACTAGTGGCGAGGCTATGGAAGAAAGGAGCAGCTGTGGAGCTGGGCT 2062
 QY 486 euLeuLeuLeuSer---LeuSerGlnGlyGlnGluCysGlyGluTyRProVal-----502
 Db 2063 GTACTGTGTGGMAATGTGTACAGAGAAACACCTTGGGAGAGATGTAAGACTATGGCTG 2122
 QY 503 -----ThrIleProSerAspLeuProAlaA 511
 Db 2123 COATTTTCAAGATGCCACCAGCTTACCAATCTCAGCTGCTCTCTCACAATCTCAGAAC 2182
 QY 511 spPheGlnAspPheLeuLysCysValCysLeuAspAspLysGluArgTrpSerProG 531
 Db 2183 ACGGAGGAGCTTCTTGTAGGGGC---ATATTTGTGGAAGCTCTGTGAGAGACCTCTCAGCTG 2239

531 InGlnLeuLeuLysHisSerPhe 538
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2240 AGCAGCTGTCCACACCACTTT 2262

RESULT 14

US-08-461-145C-5
Sequence 5, Application US/08461145C
Patent No. 6074861
GENERAL INFORMATION:
APPLICANT: JOHNSON, GARY L.
TITLE OF INVENTION: NOVEL MEKK PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive and Cockfield, LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,145C
FILING DATE: 5-JUNE-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,254
FILING DATE: 11-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/323,460
FILING DATE: 14-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/11690
FILING DATE: 14-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04178
FILING DATE: 15-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/354,516
FILING DATE: 21-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kara, Catherine J.
REGISTRATION NUMBER: P-41,106
REFERENCE/DOCKET NUMBER: CPI-004CNI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3089 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 400..2280
US-08-461-145C-5

Alignment Scores:	2.38e-18	Length:	3089
Pred. No.:	284.50	Matches:	125
Score:	39.89%	Conservative:	86
Percent Similarity:	23.81%	Mismatches:	211
Best Local Similarity:	23.63%	Indels:	107
Query Match:	3.33%	Gaps:	20
	3		

115-08-461-145C-5 (1-3089)

77 valLysCysProProThrTyrProAspValValProGluIleGlu-----LeuLys 93

800 CTGGAGTGTCCAGCGAGTTCGGATCAAGCTCTCCAGTCTGCAGGGGATATAATACCA 859
 94 AsnAlaLysGlyLeuSerAsnGluSerValAsnLeuLeuLysArgLeuGluGluLeu 113
 860 TCTACCAAGCTCTCAGCCCAAGACGAGCACCTGTCTGTCA----- 901
 114 AlaLysLysHisCybGlyGluValMetIlePheGluLeuAlaTyrHisValGlnSerPhe 133
 902 GCTCCCAAGAACCTGGCCGAAGCTCTCTCCCCCGG-----GATATGTATC 946
 134 LeuSerGluHisAsnLysProProLysSer-PheHisGluGluMetLeuGluArg 153
 947 CTGAGCGCAACACAGCACATTCGCCGCAAGATCCTATACGAGCATCAACAGCGAAGTGC 1006
 153 gAlaGlnGluGlnGlnArgLeuLeuGluAlaLys-----ArgLysG1 168
 1007 AATTCTATCCAGAGACCGACGACAGTGTATGTCTAGATCCCTCAGCAGTCCGCAAAATT 1066
 168 uGluGlnGluArgGluIleLeuHisGluIleGlnArg-LysGluGluIleLysG 188
 1067 CCTTGTTCAGGAAGCTGCCAATCTCTGGACAGGTCTAGCAGACAGGCCATCTCTCAGGAAT 1126
 188 luGluLysLysArgLysGluMetAlaLysGlnArgLeuGluIleAlaSerLeuSerA 208
 1127 CACAAATGTCCCGAGCCCGGAGTCTCCAGACACACAGAAAGAAATGCTCAGATCGGAGA 1186
 208 snGlnAspHisThrSerLysLysAspProGlyGly-----HisArgThrAlaAlaI 225
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 261 erProGlySerCysGluIleLeuTyr-PheAsnMetGlySerProAspGlnLeuMetValH 281
 1331 CAAAGTCGCTCTGAGACAAATGGCCAGAAACATGGTGTAGTGTGCAATACCTGGACC 1390
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 292 -----LeuGlyLysLeuValTyrAsnA 299
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 1504 -----CGTCAAGGTGCTTCGGCAGGGTCTAC-----TTGTGTATGATG 1543
 319 ysLysMetGlyProPheLeuThrSerGlnGluLysGlu-----LysIleAspLys 336
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 336 ysLysLysGlnIleGlnGlyThrGluThrGluPheAsnSerLeuValLysLeuSerHisP 356
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 1664 AGGCATTTGTGAGTACTACGGCTGC--CTCGGGGACCGTGTGAGAGATCTCTCACC- 1719
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 1720 --ATCTTTTGGAGTATATGCCAGGGGGCTCTGTAAAGACACAGTTGAAGCGCTACGGAG 1777
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US-09-515-806A-2 (1-1649) x US-08-628-829-9 (1-3089)

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QY	94	AsnAlaIysGlyIeuSerAsnGluSerValAsnLeuLeuLysSerArgLeuGluGluLeu	113
Db	860	TCTACCAAGTCTCTGAGCCCGAGCAGCAGCACCTGCTCTGCA	901
QY	114	AlaIysLysHisCySGlyGluValMetIlePheGluLeuAlaTyHisValGlnSerPhe	133
Db	902	GCTCCCAAGACCTGGCCGAGCTCTCTCCCCCGG	-----GATATGTAC 946
QY	134	LeuSerGluHisAsnLysProProLysSer-PheHisGluGluMetLeuGluArgAr	153
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Db	1007	AATTCAATCCAGAGCAGCGAACAGTGTATGCTAGATCCCTCAGCAGTCCGAAAATT	1066
QY	168	uGluGlnGluGlnArgGluIleLeuHisGluIleGlnArgArg-LysGluGluLysG	188
Db	1067	CCTTGTTCAGGAAGTCCCAATCTTTGGACAGGTGAGCAGCAGCCCATCTTTCAGGAAT	1126
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QY	261	erProGlySerCySGluIleLeuTyPheAsnMetGlySerProAspGlnLeuMetValH	281
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Db	1664	AGCCATTGTGCATCTACCGGTGC-----CTCGGGACCGTGTGAGAGATCTCTCACC-	1719
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us-09-515-806a-2.rni

Thu Jun 12 14:34:04 2003

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Search completed: June 12, 2003, 08:33:25
Job time : 13129 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 12, 2003, 04:43:30 ; Search time 937 Seconds
(without alignments)
2463.007 Million cell updates/sec

Title: US-09-515-806A-2

Perfect score: 8544

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Searched: 870385 seqs, 699768693 residues

Total number of hits satisfying chosen parameters: 1740770

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database :

Published Applications NA:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	8319.5	97.4	4989	9	US-09-842-758-3
3	4295	50.3	2946	9	US-09-836-392-6
4	3029	35.5	2200	10	US-09-925-301-184

Alignment Scores:
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Best Local Similarity: 100.00%
Query Match: 100.00%
Length: 5525
Matches: 1649
Conservative: 0
Mismatch: 0
Indels: 0

ALIGNMENTS

RESULT 1

US-09-515-806-1
; Sequence 1, Application US/09515806
; Patent No. US20020132321A1
; GENERAL INFORMATION:

; APPLICANT: COOK, WILLIAM J.
; TITLE OF INVENTION: 14790. NOVEL PROTEIN KINASE MOLECULE AND USES THEREFOR
; FILE REFERENCE: 38155-20002.00
; CURRENT APPLICATION NUMBER: US/09/515, 806
; CURRENT FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 5525
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (63)..(4991)
US-09-515-806-1

Sequence 117, App
Sequence 753, App
Sequence 24436, A
Sequence 1, Appli
Sequence 101, App
Sequence 12737, A
Sequence 105, App
Sequence 18, Appl
Sequence 103, Appl
Sequence 16, Appl
Sequence 107, App
Sequence 3, Appli
Sequence 1707, Ap
Sequence 23, Appl
Sequence 147, App
Sequence 298, App
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Sequence 2146, Ap
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Sequence 7309, Ap
Sequence 11, Appl
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Sequence 14, Appl
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Thu Jun 12 14:34:05 2003

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 4743 TCCCTTGGCACTTACATCAGAAAGCAGTGTGAAATTTGAAATTTGAAATTTGAAAT 4802
 1581 LysGluThrIleLeuGlnPheLeuSerLeuGluThrAspAlaLeuGlnAlaPheAsn 1600
 4803 AAGAAACAATATTACAGTGTGTTTATCATTTAGAGTGGATGCTGATGACAGGATTAAC 4862
 1601 ThrThrValLysGlnLeuSerArgLeuProLysGlnArgTyrLeuLysLeuValCys 1620
 4863 ACAACTGTGAACAGCTGCTGTCTACGCTGCTGCAAGCAAGATACCTCAAAATTAGTCTGT 4922
 1621 AspGluLeuTyrAsnIleLysValGluLysValSerValLeuPheLeuTyrSerTyr 1640
 4923 GATGAATTTATAACATCAAGTGAAGAAAAAGGTTGCTGTCTATTCTGTACAGCTAT 4982
 1641 ArgAspAspTyrTyrArgIleLeuPhe 1649
 4983 AGAGATGACTACTACAGAAATCTATT 5009

US-09-515-806A-2 (1-1649) x US-09-842-758-3 (1-4989)
 QY 1 MetAlaGlyGlyArgGlyAlaProGlyValArgGlyArgGlyProGluSerTyrPro 20
 Db 1 ATGGCTGGGGCGCGTGGGGCGCGCGGGCGCGCGGGCGCGCGGGCGCGGGCGCGGG 60
 QY 21 GlnArgGlnAspHisGluLeuGlnAlaLeuGluAlaIleTyrGlyAlaAspPheGlnAsp 40
 Db 61 CACAGACAGAGACACAGAGCTACAGGCGCTGGAGGCGCATCTACGGCGCGGACTTCCAGAC 120
 QY 41 LeuArgProAspAlaCysGlyPro-----ValLysGluProProGluIleAsnLeuVal 58
 Db 121 CTGCGCGCGGCGCTTGGCGACCGGTAAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 180
 QY 59 LeuTyrProGlnGlyLeuThrGlyGluGluValTyrValLysValAspLeuArgValLys 78
 Db 181 TTGTACCCCTCAAGCCCTAACTGTGTGAAGAAGTATATGTAAAGAGTGGATTGAGGGTTTAA 240
 QY 79 CysProProThrTyrProAspValValProGluIleGluLeuLysAsnAlaLysGlyLeu 98
 Db 241 TGCCACCTACCTATCCAGATGTAGTTCCTGAAATAGAGTTAAAAAATGCCAAAGGTCTTA 300
 QY 99 SerAsnGluSerValAsnLeuLeuLysSerArgLeuGluGluLeuAlaLysHisCys 118
 Db 301 TCAATGAAAGTGTCAATTTGTTAAATCTCGCTAGAGAGAGAGAGAGAGAGAGAGAGAG 360
 QY 119 GlyGlu---ValMetIlePheGluLeuAlaTyrHisValGlnSerPheLeuSerGluHis 137

RESULT 2
 US-09-842-758-3
 ; Sequence 3, Application US/09842758
 ; Publication No. US20030083244A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Vernet, Corine A. M.
 ; APPLICANT: Fernandes, Elma R.
 ; APPLICANT: Gerlach, Valerie
 ; APPLICANT: Shimkets, Richard A.
 ; APPLICANT: Malyankar, Uriel M.
 ; APPLICANT: Boldog, Ferenc L.
 ; APPLICANT: Zerhusen, Bryan D.
 ; APPLICANT: Spytek, Kimberly A.
 ; APPLICANT: Majumder, Kumud
 ; APPLICANT: Tchernev, Velizar T.
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Burgess, Catherine E.
 ; APPLICANT: Gangolli, Esha A.
 ; APPLICANT: Smithson, Glenda
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: MacDougall, John R.
 ; APPLICANT: Taupier, Raymond J.
 ; APPLICANT: Grosse, William M.
 ; APPLICANT: Edward, Szekeres S.
 ; APPLICANT: Alsobrook II, John P.
 ; FILE OF INVENTION: No. US20030083244A1el Proteins and Nucleic Acids Encoding Same
 ; TITLE REFERENCE: 15966-783
 ; CURRENT APPLICATION NUMBER: US/09/842,758

Db	361	GGGGAGGTAGTGTATGATCTTTTGAACCTGGCTTACCACGTGGCAGTCAITTTCTCAGCGGACAT	420
Qy	138	AsnLysProProProLysSerPheHisGluMetLeuGluArgArgAlaGlnGluGlu	157
Db	421	AACAAGCCCTCCCAAGTCTTTTCATGAAGAAATGCTGGAAAGCGGCTCAAGAGGAG	480
Qy	158	GlnGlnArgLeuLeuGluAlaLysArgLysGluGluGlnGlnArgGluLeuHis	177
Db	481	CAACACAGAGCTGTTGGAGCCCAAGCGAAGAGACACACAGCTGAATCTCGCAT	540
Qy	178	GluLeuGlnArgArgLysGluGluLeuLysGluGluLysArgLysGluMetAlaLys	197
Db	541	GAGATTACAGAGAGGAAGAGAGATATAAAGAGAGAAAAAGGAAAGAAATGGCTAAG	600
Qy	198	GlnGluArgLeuGluLeuAlaSerLeuSerAsnGlnAspHisThrSerLysLysAspPro	217
Db	601	CAGAAACGTTTGGAAATGCTAGTTTGTCAACCAAGATCATACCTCTAAGAGAGACCCA	660
Qy	218	GlyGlyHisArgThrAlaAlaLeuHisGlyGlySerProAspPheValGlyAsnGly	237
Db	661	GGAGGACACAGACGGCTGCCATTCTACATGGAGGCTCTCCTGACTTTGTAGGAATGGT	720
Qy	238	LysHisArgAlaAsnSerSerGlyArgSer-----ArgArgGluArgGlnTyrSerVal	255
Db	721	AAACATCGGCAACCTCTCAGAAAGCTAGGTTAAGCGAGAACGTCAGTATTTCTGTA	780
Qy	256	CysAsnSerGluAspSerProGlySerCysGluLeuLeuTyrPheAsnMetGlySerPro	275
Db	781	TGTAATAGTGAAGATTCTCTGGCTTTGTGAAATTCGTATTTCAATATGGGAGTCTCT	840
Qy	276	AspGlnLeuMetValHisLysGlyLysCysIleGlySerAspGluGlnLeuGlyLysLeu	295
Db	841	GATCAGCTCATGGTGCACAAAGGAAATGATTGGCAGTGATGAACAATTCGGAATAA	900
Qy	296	ValTyrAsnAlaLeuGluThrAlaThrGlyGlyPheValLeuLeuTyrGluTyrValLeu	315
Db	901	GTCTACAATGCTTTGGAAACAGCCACCTGGTGGCTTTGTCTTTGTATGAGTGGGTCTT	960
Qy	316	GlnTyrGlnLysLysMetGlyProPheLeuThrSerGlnGluLysGluLysIleAspLys	335
Db	961	CAGTGGCAGAAAAAATGGGTCCATTCCTTACCAGTCAAGAAAAAGAGAAATTTGATAAG	1020
Qy	336	CysLysLysGlnIleGlnGlyThrGluThrGluPheAsnSerLeuValLysLeuSerHis	355
Db	1021	TGCAAAAGCAGATTCAAGAACAGAAACAGAAATCAACTCACTGGTAAAAATTGAGCCAT	1080
Qy	356	ProAsnValValArgTyrLeuAlaMetAsnLeuLysGluGlnAspAspSerIle-ValVa	375
Db	1081	CCAATGTAGTACGTACCTTGCATTAATTC- AAAGAGCAAGACGACTCCATTCGTGGT	1139
Qy	375	LspIleLeuValGluHisLysSerClyValSerLeuAlaHisLeuSerHisSerGly	395
Db	1140	GGCAATTTAGTGGACACATTAGTGGGGTCTCTCTTCTGTCACACCTGAGCCACTCAGG	1199
Qy	395	YProIleProValHisGlnLeuArgTyrThrAlaGlnLeuLeuSerClyLeuAspTyr	415
Db	1200	CCCCATCCCTGTGCATCAGCTTCGCAGGTACACAGCTCAGCTCTCTGTAGGGCTTCGATTA	1259
Qy	415	rIleHisSerAsnSerValValHisLysValLeuSerAlaSerAsnValLeuValAspAl	435
Db	1260	TCTGCACAGCAATTCGTGGTGCATTAAGGTCCTGAGTGATCTTAATGTCTTGGTGGATGC	1319
Qy	435	aGluGlyThrValLysIleThrAspTyrSerIleSerLysArgLeuAlaAspIleCysLys	455
Db	1320	AGAGGACCCGTCAAGATTACGGACTATAGCAATTCAGCCGCTCGCAGACATTTGCA	1379
Qy	455	eGluAspValPheGluGlnThrArgValArgPheSerAspAsnAlaLeuProTyrLysTh	475
Db	1380	GGAGGATGTGTTTCAGCAAAACCGAGTTCGTTTTAGTGACAATGCTCTGCCTTATAAAC	1439
Qy	475	rGlyLysLysGlyAspValTrpArgLeuGlyLeuLeuLeuLeuSerLeuSerGlnGlyGI	495
Db	1440	GGGAGAGAAAGGAGATGTTGGCGTCTTGGCCTCTCTGCTGTCTTCCCTCAGCCAGGACA	1499

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QY	854	ePheLeuAspSerAspAspHisVallylleGlyAspPheGlyLeuAlaThrAspHisLe	874	Db	3657	GATCCCAAGAGATAACTCAGTCAAGTCTACATTATCTGTATGATGCTGTGCACAGAA	3716
Db	2577	TTTTTTGGATTCTGATGACCATGTGAAATAGGTGATTTTGGTTGGCGACAGCACTCT	2636	QY	1234	sLeuThrArgArgGluValGluAlaLysPheCysAsnLeuSerLeuSerSerAsnSerLe	1254
QY	874	uAlaPheSerAlaAspSerLysGlnAspAspGlnThrGlyAspLeuLysSerAspPr	894	Db	3717	GCTGACGAGGAGAGAGTGAAGCTAAATTTTGTAAATCTGTCTTTCTTAATAGTCT	3776
Db	2637	AGCCTTTTCTGCTGACACCAACCAAGACGATCAGACAGAGAGCTTGAATTAAGTCAGACCC	2696	QY	1254	uCysArgLeuTyrLysPheLleGluGlnLysGlyAspLeuGlnAspLeuMetProThrIrl	1274
QY	894	oSerGlyHisLeuThrGlyMetValGlyThrAlaLeuTyrValSerProGluValGlnG	914	Db	3777	GTGTCGACTCTACAGTTTATTGAAACAGAGGGAGATTTCGAAGATCTTATGCCCTTAAAGA	3836
Db	2697	TTTCAGGTCACTTAACCTGGGATGTTGGCACTCTCTATGTAAGCCAGAGTCCCAAG	2756	QY	1274	eAsnSerLeuLysGlnLysThrGlyLleAlaGlnLeuValLysTyrGlyLeuLysAs	1294
QY	914	ySerThrLysSerAlaTyrAsnGlnLysValAspLeuPheSerLeuGlyLlePhePh	934	Db	3837	AAATTCATTAATAGAACAGAAACAGAGTATTCGACAGTGTGTGAAGTATGCTTAAAGA	3896
Db	2757	AAGCACCATAATCTGCATACACACAGAAAGTGGATCTCTTCAGCCCTGGGAATATCTTCT	2816	QY	1294	pLeuGluGluValValGlyLeuLeuLysLysLeuGlyLleLysLeuGln-----Valle	1312
QY	934	eGluMetSerTyrHisProMetValThrAlaSerGluArgLlePheValLeuAsnGlnLe	954	Db	3897	CCTAGAGGAGGTGTGGACTGTGGAAGAACTCGGCATCAAGTTACAGGTTTGGGTCCT	3956
Db	2817	TGAGATGCTCTATCACCCATGCTGACGGCTTCAGAAAGGATCTTGTCTCAACCAACT	2876	QY	1312	uLleAsnLeuGlyLeuValTyrLysValGlnGlnHisAsnGlyLleLlePheGlnPheVa	1332
QY	954	uArgAspProThrSerProLysPheProGluAspPheAspAspGlyGluHisAlaLysG	974	Db	3957	GATCAATTTGGGCTTGGTTTACAAGGTGCAGCAGCACAATGAATCATCTTCCAGTTTGT	4016
Db	2877	CAGAGATCCCACTTCGCTTAAGTTTCCAGAGACTTTGACAGATGGAGAGCATGCAAGCA	2936	QY	1332	lAlaPheLleLysArgArgGlnArgAlaValProGluLleLeuAlaAlaGlyGlyArgTy	1352
QY	974	nLysSerValLleSerTrpLeuLeuAsnHisAspProAlaLysArgProThrAlaThrGl	994	Db	4017	GGCTATCATCAACGAAGGCAAGGCTGTACCTGAAATCTCTCGCAGCTGGAGGAGATA	4076
Db	2937	GAATCAGTCATCTCTCGCTGCTGTTGAACCAACGATCCAGCAAAACGGCCACAGCACA	2996	QY	1352	rAspLeuLeuLleProGlnPheArgGlyProGlnAlaLeuGlyProValProThrAlaAl	1372
QY	994	uLeuLeuLysSerGluLeuLeuProProProGlnMetGluGluSerGluLeuHisGluVa	1014	Db	4077	TGACTGCTGATTCCTCCAGTTTGAAGGGCCACAAGCTCTGGGGCCAGTTCCCACTGCCAT	4136
Db	2997	ACTGCTCAAGAGTGAAGTCTGCTGCCCCACCCAGATGGAGAGTCAGAGCTGCATGAAGT	3056	QY	1372	eGlyValSerLleAlaLleAspLysLleSerAlaAlaValLeuAsnMetGluGlu-----	1390
QY	1014	lLeuHisHisThrLeuThrAsnValAspGlyLysAlaTyrArgThrMetMetAlaGlnIl	1034	Db	4137	TGGGGTCAAGCATAGCTATGACAGATATCTGCTGCTGCTCTCAACATGGAGAAATCTGT	4196
Db	3057	GCTGCACCAACAGCTGACCAACAGTGGATGGAGGCTTACCGACCATGATGGCCCAT	3116	QY	1391	----SerValThrLleSerSerCysAspLeuLeuValSerValGlyGlnMetSerMe	1409
QY	1034	ePheSerGlnArgLleSerProAlaLleAspTyrThrTyrAspSerAspLleLeuLysG	1054	Db	4197	AGTCTGTTTACAATAGGCTCTGGGGACCTCTGGTTGTAAAGTGTGGCCAGATGTCTAT	4256
Db	3117	CTTCTCGCAGCATCTCCCTGCCATTCGATTAACCTATGACAGGAGATCTGAAAGG	3176	QY	1409	tSerArgAlaLleAsnLeuThrGlnLysLeuTyrThrAlaGlyLleThrAlaGluLleMe	1429
QY	1054	yAsnPheSerLleArgThrAlaLysMetGlnGlnHisValCysGluThrLleLleArgIl	1074	Db	4257	GTCAGGGCCATAAACCTTAACCCAGAAACTCTGGACAGCAGGCATACAGCAGAAATCAT	4316
Db	3177	CAACTTCTCAATCCGTACAGCAGCAAGATGCAGCAGCATGTGTGAAACCATCATCCGCAT	3236	QY	1429	tTyrAspTrpSer-----GlnSerGlnGluGluGlnGluTyrCysArgHisHisG	1447
QY	1074	ePheLysArgHisGlyAlaValGlnLeuCysThrProLeuLeuLeuProArgAsnArgG	1094	Db	4317	GTACGACTGTGTACAGATTTTCAGTCCCAAGAGAGAAATTACAGAGTACTGCAGACATCATG	4376
Db	3237	CTTTAAAGACATGGTGTGTTTCAGTGTGTACTCCACTACTGCTTCCCCGAAACAGACA	3296	QY	1447	uLleThrTyrValAlaLeuValSerAspLysGluGlySerHisValLysValLysSerPh	1467
QY	1094	nLleTyrGluHisAsnGluAlaLleLeuPheMetAspHisSerGlyMetLeuValMetLe	1114	Db	4377	AATCACCTATGTGGCCCTTGTCTCGGATAAAGAGAAAGCCATGTCAAGGTTAAAGTCTTT	4436
Db	3297	AATATATGACACCAACGAAGCTGCCCTATTTCATGGACACACAGCGGATGCTGGTGTGCT	3356	QY	1467	eGluLysGluArgGlnThrGluLysArgValLeuGluThrGluLeuValAspHisValLe	1487
QY	1114	uProPheAspLeuArgLleProPheAlaArgTyrValAlaArgAsnAsnLleLeuAsnLe	1134	Db	4437	CGAAGAGAAAGGCAGACAGAGAGCGTGTCTGGAGACTGAACTTGTGGACCATGTACT	4496
Db	3357	TCCTTTGACCTGGGGTGGCTTTTGCAAGATATGGCAAGAAATATATATTGAATTT	3416	QY	1487	uGlnLysLeuArgThrLysValThrAspGluArgAsnGlyArgGluAlaSerAspAsnLe	1507
QY	1134	uLysArgTyrCysLleGluArgValPheArgProArgLysLeuAspArgPheHisProly	1154	Db	4497	GCAGAAACTGAGAGCTAAAGTCACTGATGAAAGAAATTTTAGAGAGAGCTTCCGATAACT	4556
Db	3417	AAAACGGTACTGCATAGAACGTGTTCACGCGCGCAAGTTAGATCGATTTTCATCCCAA	3476	QY	1507	uAlaValGlnAsnLeuLysGlySerPheSerAsnAlaSerGlyLeuPheGluLleHisG	1527
QY	1154	sGluLeuLeuGluCysAlaPheAspLleValThrSerThrAsnSerPheLeuProTh	1174	Db	4557	TGCAGTGCATAATCTGAAAGGGGTCAATTTCTAATGCTTCAGGTTTCTTTGAAATCCATCG	4616
Db	3477	AGAACTTCGGAGTGTGCTTTGATATTGTCACTTCTACCAACCAACAGCTTTCGCCAC	3536	QY	1527	yAlaThrValValProLleValSerValLeuAlaProGluLysLeuSerAlaSerThrAr	1547
QY	1174	rAlaGluLleLleTyrThrLleTyrGluLleGlnGluPheProAlaLeuGlnGluAr	1194	Db	4617	AGCAACAGTGGTTCCTCAATGTTGTAGTGTGTAGCCCGGAGAGGCTGTACCCAGCACTAG	4676
Db	3537	TGCTGAAATTAATCTACACTATCTATGAAATCATCAAGAGTTTCCAGCACTTCAAGAAAG	3596	QY	1547	gArgArgTyrGluThrGlnValGlnThrArgLeuGlnThrSerLeuAlaAsnLeuHisG	1567
QY	1194	gAsnTyrSerLleTyrLeuAsnHisThrMetLeuLysAlaLleLeuLeuHisCysG	1214	Db	4677	GAGCGCTATGAAACTCAGGTACAACTCGACTTCAGACCTCCCTGCCAATCTTACATCA	4736
Db	3597	AAATTACAGTATTATTGTAACCATCACTGATTTTGAAGCAATACTCTTACACTGTGG	3656	QY	1567	nLysSerSerGluLleGluLleLeuAla---ValAspLeuProLysGluThrLleLeuG	1586
QY	1214	yLleProGluAspLysLeuSerGlnValTyrLleLleLleTyrAspAlaValThrGluLy	1234				

Db 4737 GAAAGACAGTGAAATGAAATTCCTGGCTGTAGTGATCTACCCAAAGAAACAATATTACA 4796
 QY 1586 nHeLeuSerLeuGluTrpAspAlaAspGluGlnAlaPheAsnThrThrValLysGlnLe 1606
 Db 4797 GTTTTATCATAGAGTGGGATGCTGATGAACAGGCAATTAAACAACTGTGAACAGCT 4856
 QY 1606 uLeuSerArgLeuProLysGlnArgTyrLeuLysLeuValCysAspGluLileTyrAsnIl 1626
 Db 4857 GCTGTCACGCTGCCAAGCAAGATACCTCAATTAATAGTCTGTGATGAATTTATAACAT 4916
 QY 1626 eLysValGluLysLysValSerValLeuPheLeuTyrSerTyrArgAspAspTyrTrAr 1646
 Db 4917 CAAAGTAGAAAAGAGTGTCTGTGCTATTCTGTACAGCTATAGAGATGACTACTACAG 4976
 QY 1646 gileLeuPhe 1649
 Db 4977 AATCTTATTT 4986

RESULT 3

US-09-836-392-6
 ; Sequence 6, Application US/09836392
 ; Patent No. US20020173458A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Protein Tyrosine Kinase Receptor Polynucleotides, Polypeptides, a
 ; FILE REFERENCE: PT020P1
 ; CURRENT APPLICATION NUMBER: US/09/836,392
 ; PRIOR FILING DATE: 2001-04-18
 ; PRIOR APPLICATION NUMBER: PCT/US00/28066
 ; PRIOR FILING DATE: 2000-10-11
 ; PRIOR APPLICATION NUMBER: 60/159,542
 ; PRIOR FILING DATE: 1999-10-15
 ; PRIOR APPLICATION NUMBER: 60/165,914
 ; PRIOR FILING DATE: 1999-11-17
 ; PRIOR APPLICATION NUMBER: 60/189,027
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 6
 ; LENGTH: 2946
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-836-392-6

Alignment Scores:
 Pred. No.: 0 Length: 2946
 Score: 4295.00 Matches: 841
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 50.27% Indels: 0
 DB: 9 Gaps: 0

US-09-515-806A-2 (1-1649) x US-09-836-392-6 (1-2946)

QY 809 ThrLeuArgAspThrIleAspGlnGlyLeuTyrArgAspThrValArgLeuTrpArgLeu 828
 Db 14 ACTTTACGAGACACCATTCAGGAGGACTGATCGAGACACCGTCAGACTCTGAGGCTT 73
 QY 829 PheArgGluLeuLeuAspGlyLeuAlaTyrIleHisGluLysGlyMetIleHisArgAsp 848
 Db 74 TTTTCGAGAGATTCTGGATGGATTAGCTATTATCATCATGAGAAAGAAATGATTCACCGGAT 133
 QY 849 LeuLysProValAsnIlePheLeuAspSerAspAspHisValLysIleGlyAspPheGly 868
 Db 134 TTGAGCCCTGTCACATTTTGGATCTGATGACCATGTGAATAGTGTATTTGGT 193
 QY 869 LeuAlaThrAspHisLeuAlaPheSerAlaAspSerLysGlnAspAspGlnThrGlyAsp 888
 Db 194 TTGGCGCAGACCATCTAGCCTTTTCTGCTGACAGCAACAAACACCATCAGACAGGAGAC 253
 QY 889 LeuLysSerAspProSerGlyHisLeuThrGlyMetValGlyThrAlaLeuTyrVal 908

Db 254 TTGATTAAAGTCAGACCCCTTCAGGTCACTTAACCTGGGATGCTTGGCACTGCTCTCTATGTA 313
 QY 909 SerProGluValGlnGlySerThrLysSerAlaTyrAsnGlnLysValAspLeuPheSer 928
 Db 314 AGCCCAAGAGTCCCAAGGAGACCAATCTGCATACCAACAGAAAGTGGATCTCTTCAGC 373
 QY 929 LeuGlyIleIlePhePheGluMetSerTyrHisProMetValThrAlaSerGluArgIle 948
 Db 374 CTGGGAATTTATCTTTCTTGGATGTCTATCACCCCATGTCAGGCTTCAGAAAGGATC 433
 QY 949 PheValLeuAsnGlnLeuArgAspProThrSerProLysPheProGluAspPheAsp 968
 Db 434 TTTGTCTCAACCACTCAGATCCCACTTCGCTTAAGTTTCCAGAAAGACTTTGACAT 493
 QY 969 GlyGluHisAlaLysGlnLysSerValIleSerTrpLeuLeuAsnHisAspProAlaLys 988
 Db 494 GGAGAGCATCAAGAGCAGAAATCAGTCATCTCTGGCTGTGAAACACGATCCAGCAAAA 553
 QY 989 ArgProThrAlaThrGluLeuLysSerGluLeuLeuProProProGlnMetGluGlu 1008
 Db 554 CGGCCACACGACACAGAACTGCTCAAGAGTGAGCTGCTGCCCTCCACCCACGATGAGGAG 613
 QY 1009 SerGluLeuHisGluValLeuHisThrLeuThrAsnValAspGlyLysAlaTyrArg 1028
 Db 614 TCAGAGCTGCATGAAGTGTGTCACACACGCTGACCAACGTTGGATGGAGGCTTACCCG 673
 QY 1029 ThrMetMetAlaGlnIlePheSerGlnArgIleSerProAlaIleAspTyrThrTyrAsp 1048
 Db 674 ACCATGATGCCCCAGATCTTCTCGCAGGCACTCTCCCTGCTGATGGAAGGCTTACCCG 733
 QY 1049 SerAspIleLeuLysGlyAsnPheSerIleArgThrAlaLysMetGlnGlnHisValCys 1068
 Db 734 AGCGACATCTGAAGGCAACTTCTCAATCGGTACACCAAGATGCAAGCATGTGTGT 793
 QY 1069 GluThrIleIleArgIlePheLysArgHisGlyAlaValGlnLeuCysThrProLeuLeu 1088
 Db 794 GAAACCATCATCCGCACTTTTAAAGACATGGAGCTGTTTCAGTTGTGTACTCCACTACTG 853
 QY 1089 LeuProArgAsnArgGlnIleTyrGluHisAsnGluAlaAlaLeuPheMetAspHisSer 1108
 Db 854 CTTCCCGAAACAGACAAATATATAGCACACAGAGCTGCCCTATTTCATGACACACAGC 913
 QY 1109 GlyMetLeuValMetLeuProPheAspLeuArgIleProPheAlaArgTyrValAlaArg 1128
 Db 914 GGGATGCTGTGATGCTTCTTTTGACCTCGCGATCCCTTTTGCAGATATATGCAAGA 973
 QY 1129 AsnAsnIleLeuAsnLeuLysArgTyrCysIleGluArgValPheArgProArgLysLeu 1148
 Db 974 AATAATATATTGAATTTAAACCGATATCTGATAGAACGTTGTTTTCAGGCCGCGCAAGTTA 1033
 QY 1149 AspArgPheHisProLysGluLeuLeuGluCysAlaPheAspIleValThrSerThrThr 1168
 Db 1034 GATCGATTTTCATCCCAAGAACTTCTGGAGTGTGATTTGATTTGTCACCTTCTACACC 1093
 QY 1169 AsnSerPheLeuProThrAlaGluIleIleTyrThrIleTyrGluIleIleGlnGluPhe 1188
 Db 1094 AACAGCTTTCTGCCACTCTCTGAATTTATCTACACTATCTATGAATCATCCCAAGATTTT 1153
 QY 1189 ProAlaLeuGlnGluArgAsnTyrSerIleTyrLeuAsnHisThrMetLeuLeuLysAla 1208
 Db 1154 CAGACATTCAGAAAGAAATTTACAGTATTATTATTTGAACCATCATGTTTATTGAAGCA 1213
 QY 1209 IleLeuLeuHisCysGlyIleProGluAspLysLeuSerGlnValTyrIleIleLeuTyr 1228
 Db 1214 ATACTCTACACTGTGGGATCCAGAGATTAATCTCAGTCAAGTCTACATTTATCTGTAT 1273
 QY 1229 AspAlaValThrGluLysLeuThrArgGluValGluAlaLysPheCysAsnLeuSer 1248
 Db 1274 GATGCTGTGACAGAGAGCTGACGAGGAGAGAGTGGAAAGCTAAATTTTGTAACTCTGTCT 1333
 QY 1249 LeuSerSerAsnSerLeuCysArgLeuTyrLysPheIleGluGlnLysGlyAspLeuGln 1268
 Db 1334 TTGCTCTCTATAGTGTGTGCTGACTCTCAAGTTTATTGAACAGAGGAGAGATTGCAA 1393

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1629 GluLysValSerValLeuPheLeuTyrSerTyrArgAspTyrTyrArgIleLeu 1648
 2474 GAAAAAAGGTGTCTGTGCTATTTCCTGATAGAGATGACTTACTACAGAATCTTA 2533

1269 AspLeuMetProThrIleAsnSerLeuIleLysGlnLysThrGlyIleAlaGlnLeuVal 1288
 1394 GATCTTATGCCAACAAATAATTCATTATAACAGAAAAACAGGTATGACAGTGGTG 1453
 1289 LysTyrGlyLeuAspLeuGluValValGlyLeuLeuLysLeuGlyIleLys 1308
 1454 AAGTATGGCTTAAAGACCTAGAGGAGGTGTGTGACTGTGTGAAGAACTCGGCATCAG 1513
 1309 LeuGlnValLeuLeuAsnLeuGlyLeuValTyrLysValGlnGlnHisAsnGlyIle 1328
 1514 TTACAGGTCTTGATCAATTTGGCTTGTGTTACAGGTTCAGAGGTGCAGCAATGGAATC 1573
 1329 PheGlnPheValAlaPheLeuLysArgGlnAlaValProGluLeuLeuAla 1348
 1574 TTCAGTTGTGGCTTTCATCAACAGAGGCAAGGCTGTACCTGGAATCTCGCAGCT 1633
 1349 GlyGlyArgTyrAspLeuLeuIleProGlnPheArgGlyProGlnAlaLeuGlyProVal 1368
 1634 GGAGGCAGATATGACCTGCTGTATCCAGTTTACAGGTTCAGAGGCAAGCTGTGGGCGAGTT 1693
 1369 ProThrAlaIleGlyValSerIleAlaIleAspLysIleSerAlaValLeuAsnMet 1388
 1694 CCCACTGGCATTTGGGTTCAGTAGCTATAGACAGATATCTGCTGCTCTCAACATG 1753
 1389 GluGlnSerValThrIleSerSerCysAspLeuValValSerValGlyGlnMetSer 1408
 1754 GAGGAATCTGTTCATTAAGCTCTGTGACCTCTGCTGTTGTAAGTGTGGCCAGATGCT 1813
 1409 MetSerArgAlaIleAsnLeuThrGlnLysLeuThrPheAlaGlyIleThrAlaGluIle 1428
 1814 ATGTCAGGGCCATCAACCTTAACAGAACTCTGGACAGCAGGCAATCAGAGAAATC 1873
 1429 MetTyrAspTrpSerGlnSerGlnGluLeuGlnGluTyrCysArgHisHisGluIle 1448
 1874 ATGTACGACTGTGTACAGTCCAGAGAGAAATTCAGAGTACTGCAGACATCATGAAATC 1933
 1449 ThrTyrValAlaLeuValSerAspLysGlySerHisValLysValLysSerPheGlu 1468
 1934 ACCTATGTGGCTTGTCTCGGATAAAGAGAAAGCCATGTCAAGGTTAAGTCTTCGAG 1993
 1469 LysGluArgGlnThrGluLysArgValLeuGluThrGluLeuValAspHisValLeuGln 1488
 1994 AAGGAAAGGCAGACAGAGAGGCTGTGTGGAGTGAACCTGTGGACCATGTACTGCAG 2053
 1489 LysLeuArgThrLysValThrAspGluArgAsnGlyArgGluAlaSerAspAsnLeuAla 1508
 2054 AAATGAGGACTAAAGTCACTGATGAAAGAAATGGCAGAGAGCTTCGATAATCTTGCA 2113
 1509 ValGlnAsnLeuLysGlySerPheSerAsnAlaSerGlyLeuPheGluIleHisGlyAla 1528
 2114 GTGCAAAATCTGAAGGGGTCAATTTCTTAATGCTTCAGTTTGTGTTGAAATCCATGGAGCA 2173
 1529 ThrValValProIleValSerValLeuAlaProGluLysLeuSerAlaSerThrArgArg 1548
 2174 ACAGTGTGTTCCATTTGAGTGTGTAGCCCGAGAGAGCTGTACAGCCAGCACTAGGAGG 2233
 1549 ArgTyrGluThrGlnValGlnThrArgLeuGlnThrSerLeuAlaAsnLeuHisGlnLys 1568
 2234 CGCTATGAACCTCAGGTACAACTTCGACTTCAGACCTCCCTTGGCAACTTACATCAGAAA 2293
 1569 SerSerGluIleGluLeuAlaValAspLeuProLysGluThrIleLeuGlnPheLeu 1588
 2294 AGCAGTGAATTTGAAATTTCTGCTGTGATCTACCCAAAGAAACAATATTACAGTTTTTA 2353
 1589 SerLeuGluTrpAspAlaAspGluGlnAlaPheAsnThrThrValLysGlnLeuLeuSer 1608
 2354 TCATTAGAGTGGGATGCTGATGAACAGGCACTTAAACAACTGTGAAGCAGCTGTGTCA 2413
 1609 ArgLeuProLysGlnArgTyrLeuLysLeuValCysAspGluIleTyrAsnIleLysVal 1628
 2414 CGCCTGCCAAAGCAAGATACCTCAAAATAGTCTGTGATGAATTTTATAACATCAAGTA 2473

RESULT 4
 US-09-925-301-184
 ; Sequence 184, Application US/09925301
 ; Patent No. US20020052308A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: PA106
 ; CURRENT APPLICATION NUMBER: US/09/925,301
 ; PRIOR FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05882
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124,270
 ; PRIOR FILING DATE: 1999-03-12
 ; NUMBER OF SEQ ID NOS: 1694
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 184
 ; LENGTH: 2200
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (2096)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc feature
 ; LOCATION: (2140)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc feature
 ; LOCATION: (2157)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc feature
 ; LOCATION: (2181)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc feature
 ; LOCATION: (2184)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; US-09-925-301-184

Alignment Scores:
 pred. No.: 1,1e-289 Length: 2200
 Score: 3029.00 Matches: 599
 Percent Similarity: 99.67% Conservative: 0
 Best Local Similarity: 99.67% Mismatches: 2
 Query Match: 35.45% Indels: 0
 DB: 10 Gaps: 0

US-09-515-806A-2 (1-1649) x US-09-925-301-184 (1-2200)
 QY 1049 SerAspIleLeuLysGlyAsnPheSerIleArgThrAlaLysMetGlnHisValCys 1068
 Db 10 AGGCACATCTCAAGGGCAACTTCTCAATCCGTCAGCCAAAGATGCAGCAGCATGTGTGT 69
 QY 1069 GluThrIleLeuArgIlePheLysArgHisGlyAlaValGlnLeuCysThrProLeuLeu 1088
 Db 70 GAAACCATCATCCGCATCTTTAAAGACATGAGGTTCAGTTGTGTACTCCACTACTG 129
 QY 1089 LeuProArgAsnArgGlnIleTyrGluHisAsnGluAlaAlaLeuPheMetAspHisSer 1108
 Db 130 CTTCCCGCAACAGACAAATATATAGCAACACAGAGCTGCCCTTATTCTATGACCACAGC 189
 QY 1109 GlyMetLeuValMetLeuProPheAspLeuArgIleProPheAlaArgTyrValAlaArg 1128
 Db 190 GGGATGCTGGTGATGCTTCCCTTTTACCTGCGGATCCCTTTTCAAGATATGTGCAAGA 249
 QY 1129 AsnAsnIleLeuAsnLeuLysArgTyrCysIleGluArgValPheArgProArgLysLeu 1148

Db 250 AATAATATATTGAATTTAAACGATCTGATAGACGTGTGTTTCAGCGCCGCAAGTTA 309
 QY 1149 AspArgPheHisProLysGluLeuLeuGluCysAlaPheAspIleValThrSerThrThr 1168
 Db 310 GATCGATTTCATCCCAAGAACTCTCGAGGTGTCATTTGATATGTCATCTTACCACC 369
 QY 1169 AsnSerPheLeuProThrAlaGluIleIleIleIleIleIleIleIleIleIleIle 1188
 Db 370 AACAGCTTTCGCGCCACTGCTGAATTTATCTACATCTATCTATGAAATCATCCAAAGAGTTT 429
 QY 1189 ProAlaLeuGlnGluArgAsnThrSerIleIleIleIleIleIleIleIleIleIle 1208
 Db 430 CCAGCACTTCAGGAAGAAATTAACAGTATTTATTTGAACCATACCATGTTATTTGAAGCA 489
 QY 1209 IleLeuLeuHisCysGlyIleProGluAspLysLeuSerGlnValIleIleIleIleIle 1228
 Db 490 ATACTCTTACACTGTGGATCCCAAGAGATAAACTCAGTCAAGTCTACATATTTCTGTAT 549
 QY 1229 AspAlaValThrGluLysLeuThrArgArgGluValGluAlaLysPheCysAsnLeuSer 1248
 Db 550 GATGCTGTGACAGAGAGCTGACGAGAGAGAGTGAAGCTAAATTTTGAATCTGTCT 609
 QY 1249 LeuSerSerAsnSerLeuCysArgLeuTyrlLysPheIleGluGlnLysGlyAspLeuGln 1268
 Db 610 TTGCTCTTAAATAGTCTGTGCTGACTCTACAAAGTTTATTTGAACAGAGGAGATTTGCAA 669
 QY 1269 AspLeuMetProThrIleAsnSerLeuIleLysGlnLysThrGlyIleAlaGlnLeuVal 1288
 Db 670 GATCTTATGCAACAATAAATTCATTAATAAACAAGAAACAGGTATTTGACAGTTGGTG 729
 QY 1289 LysTyrlGlyLeuLysAspLeuGluValValGlyLeuLeuLysLysLeuGlyIleLys 1308
 Db 730 AAGTATGGCTTTAAAGACCTAGAGAGGTGTGTGACTGTGTAAGAAACTCGGCATCAAG 789
 QY 1309 LeuGlnValLeuIleAsnLeuGlyLeuValTyrlLysValGlnGlnHisAsnGlyIleIle 1328
 Db 790 TTACAGCTCTGATCAATTTGGCTTGGTTTACAGGTGACAGGACCAATGGGAATCATC 849
 QY 1329 PheGlnPheValAlaPheIleLysArgArgGlnArgAlaValProGluIleLeuAlaAla 1348
 Db 850 TTCCAGTTTGTGGCTTTTCATCAACAGGCAAGGCTGTACCTGAAATCTCGCAGYT 909
 QY 1349 GlyGlyArgTyrlAspLeuLeuIleProGlnPheArgGlyProGlnAlaLeuGlyProVal 1368
 Db 910 CGAGGCAGATGATGACTCTGCTGATCCCGAGTTTACAGGGCCACAGCTCTGGGGCCAGTT 969
 QY 1369 ProThrAlaIleGlyValSerIleAlaIleAspLysIleSerAlaAlaValLeuAsnMet 1388
 Db 970 CCCACTGCCATTTGGGGTCCAGATAGTATAGCAAGATATCTGCTGCTGCTCAACATG 1029
 QY 1389 GluGluSerValThrIleSerSerCysAspLeuLeuValValSerValGlyGlnMetSer 1408
 Db 1030 GAGGAATCTGTACAAATAGCTCTGTGAGCTCTGTTGAGTGTAAAGTGTGTGTCAGATGCT 1089
 QY 1409 MetSerArgAlaIleAsnLeuThrGlnLysLeuThrAlaGlyIleThrAlaGluIle 1428
 Db 1090 ATGTCACAGGGCCATCAACCTAACCCAGAACTCTGGACAGGACGCATCACAGCAATC 1149
 QY 1429 MetTyrlAspTrpSerGlnSerGlnGluLeuGluGluTyrlCysArgHisGluIle 1448
 Db 1150 ATGTACCACTGGTCCAGAGTCCCAAGAGGAAATTAACAAGTACTGTCAGACATCATGAAATC 1209
 QY 1449 ThrTyrlValAlaLeuValSerAspLysGluGlySerHisValLysValLysSerPheGlu 1468
 Db 1210 ACCTATGGCCCTTGTCTCGGATAAAGAGAGGACCATGTCAAGTTAAGTCTTTCGAG 1269
 QY 1469 LysGluArgGlnThrGluLysArgValLeuGluThrGluLeuValAspHisValLeuGln 1488
 Db 1270 AAGGAAGGCAGACAGAGAGCGTGTGCTGGAGACTGAACTTGTGACCATGTACTGAC 1329
 QY 1489 LysLeuArgThrLysValThrAspGluArgAsnGlyArgGluAlaSerAspAsnLeuAla 1508

Db 1330 AAACCTAGGACTAAAGTCACTGATGAAGGAATGGCAGAGAAAGCTTCCGATATCTTGCA 1389
 QY 1509 ValGlnAsnLeuLysGlySerPheSerAsnAlaSerGlyLeuPheGluIleHisGlyAla 1528
 Db 1390 GTGCAAAATCTGAAGGGGTCAATTTCTAATGCTTTCAGGTTTGTGAAATCCATGGAGCA 1449
 QY 1529 ThrValValProIleValSerValLeuAlaProGluLysLeuSerAlaSerThrArgArg 1548
 Db 1450 ACAGTGGTTCCTCATTTGAGTGTGCTAGCCCGGAGAAAGCTGTCCAGCCAGCACTAGGAGG 1509
 QY 1549 ArgTyrlGluThrGlnValGlnThrArgLeuGlnThrSerLeuAlaAsnLeuHisGlnLys 1568
 Db 1510 CGGTATGAAACTCAGGTACAACTGACCTTCAGACTCCCTTGCCCACTTACATCAGAAA 1569
 QY 1569 SerSerGluIleGluIleLeuAlaValAspLeuProLysGluThrIleLeuGlnPheLeu 1588
 Db 1570 AGCAGTGAATTTGAAATTTCTGGCTGTGGATCTTACCAAGAAACAATATTACAGTTTTTA 1629
 QY 1589 SerLeuGluTrpAspAlaAspGluGlnAlaPheAsnThrThrValLysGlnLeuLeuSer 1608
 Db 1630 TCATTAGAGTGGATGCTGATGAACAGGCATTTAACACAACTGTGAACAGCTGCTGTCA 1689
 QY 1609 ArgLeuProLysGlnArgTyrlLeuLysLeuValCysAspGluIleTyrlAsnIleLysVal 1628
 Db 1690 CGCCTGCCAAAGCAAGATACCTCAATTAGTCTGTGATGAAATTTATAACATCAAGTA 1749
 QY 1629 GluLysLysValSerValLeuPheLeuTyrlSerTyrlArgAspAspTyrlArgIleLeu 1648
 Db 1750 GAAAAAAGGTGCTGTGCTCTATTCTGTACAGCTATAGATGACTACTACAGAATCTTA 1809
 QY 1649 Phe 1649
 Db 1810 TTT 1812

RESULT 5

US-09-801-368-117
 ; Sequence 117, Application US/09801368
 ; Patent No. US20020128250A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Busby, Robert
 ; APPLICANT: Cali, Brian
 ; APPLICANT: Hecht, Peter
 ; APPLICANT: Holtzman, Doug
 ; APPLICANT: Madden, Kevin
 ; APPLICANT: Maxon, Mary
 ; APPLICANT: Milne, Todd
 ; APPLICANT: No. US20020128250A1man, Thea
 ; APPLICANT: Royer, John
 ; APPLICANT: Salama, Sofie
 ; APPLICANT: Sherman, Amir
 ; APPLICANT: Silva, Jeff
 ; APPLICANT: Summers, Eric
 ; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
 ; FILE REFERENCE: 109272.147
 ; CURRENT APPLICATION NUMBER: US/09/801,368
 ; PRIOR FILING DATE: 2001-03-07
 ; PRIOR APPLICATION NUMBER: US 09/487,558
 ; PRIOR FILING DATE: 2000-01-19
 ; PRIOR APPLICATION NUMBER: US 60/160,587
 ; NUMBER OF SEQ ID NOS: 440
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 117
 ; LENGTH: 4980
 ; TYPE: DNA
 ; ORGANISM: Saccharomyces cerevisiae
 US-09-801-368-117

Alignment Scores:

Pred. No.: 4,67e-112 Length: 4980
 Score: 1242.00 Matches: 462
 Percent Similarity: 43.09% Conservative: 302
 Best Local Similarity: 26.06% Mismatches: 682

QY 339 GlnIleGlnGlyThrGluThrGluPheAsnSerLeuValLysLeuSerHisProAsnVal 339
Db 904 GAATATGCAAAATTAGAGAAAGAGTTAGAGACGGTGTGAAAGCTAAGCATACCAATGTG 963
QY 359 ValArg-----TyrLeuAlaMetAsnLeuLysGluGlnAspAspSerIleVal--- 374
Db 964 AATCGATTGTTTCGGTTATACCGTGGAGCGCATGGGAGAAATAATCAACGTTTGTGTGG 1023
QY 375 ---ValAspIleLeuValGluHisIleSerGlyValSerLeuAlaAlaHisLeuSerHis 393
Db 1024 AAAATPAGACTCTTGACAGAGTACTGTAACTACTATCCATTGGGAGATTGTACACAATCT 1083
QY 394 SerGlyProIleProValHisGlnLeuArgArgTyrThrAlaGlnLeuLeuSerGlyLeu 413
Db 1084 GTTGATTGTTAACTTAGCAACACGCGTATTGGATGATTAGATTGCTTTGAAGGATTG 1143
QY 414 AspTyrLeuHisSerAsnSerValValHisLysValLeuSerSerAlaSerAsnValLeuVal 433
Db 1144 GAGGCCATACACAAATTGGGAATTGTTCAATAATGTATCAACTTAGAAACCGGTATCCTG 1203
QY 434 -----AspAlaGluGlyThrValLysIleThrAspTyrSer-IleSerLysAr 449
Db 1204 GTGAGGATGCGAATTTTGGAGACACTATCCCAAGTAGTACTCACTCACTTATGGCTAC 1263
QY 449 GlnLeuAlaAspIleCysLysGluAspValPheGluGlnThrArgValArgPheSerAsp-- 468
Db 1264 ACTGTTTGAATATGCTATCGAGATATCCAAATAAAAAATGGTTCTTCGGTTGATTAATCT 1323
QY 469 -----AsnAlaLeuProTyrLysThrGlyLysLys 478
Db 1324 CCAAGTACATGATAGCCCTCGAGTTGTTGAAATTCATAACGCC-AAACCTCAAGATT 1382
QY 478 sGlyAspValTrpArgLeuGlyLeuLeuLeuSerLeuSerGlnGlyGlnGluCysG1 498
Db 1383 AACTGATATTGCGCACTTGGTGTGTTTATCCAGATAATCACTAGTGGAATCTGAT---- 1437
QY 498 yGluTyrProValThrIleProSerAspLeuProAlaAspPhe----- 512
Db 1438 -----ATAGTGATGAATTTTGAACCGCTCAAGNAITCCTAGATTCAACAAGTAT 1487
QY 513 -----GlnAspPheLeuLysLysCysValCysLeuAspAspLysGluuArgTr 528
Db 1488 GGATGAACCTTTATATGATCTCTTCGAAAAATGCTTAAATAACGATCCGAAGAAAAGATT 1547
QY 528 pSerProGlnGlnLeuLeuLysHisSerPheIleAsnProGln-----Pr 543
Db 1548 AGGAACATTTAGAACTACTGCCCATGAAATCTTAAGGCCAATATTGACTCTACAATCAA 1607
QY 543 oLysMetProLeuValGluGlnSer-----ProGluAs 554
Db 1608 TCGATTAACTTAGTTTCGAAAGTGTCAAATCTTAATCTCTGGAGTTAACTCTCGGAGA 1667
QY 554 p-----SerGlyGlyGlnAspTyrValGluThrValIleProSerAs 568
Db 1668 TACCATAACCGTTTCGGGCAATGAGGTAGAACACCTTCACATCGAGTATACGAAGAAG 1727
QY 568 nArgLeuProSerAlaAlaPhePheSerGlu---ThrGlnArgGlnPheSerArgTyrPh 587
Db 1728 ATCATTTAATGTTGGTCCAGATTCTCTCTATAAAATCTCGCAACGGATCAGATATGC 1787
QY 587 eileGluPheGluGluLeuGlnLeuLeuGlyLysGlyValAlaPheGlyAlaValIleLysVa 607
Db 1788 TTCTCAGCTTGAAGAGATTGCAATTTAGCCAGGCGCATTTGGACAAGTTGTCGAAGGC 1847
QY 607 lGlnAsnLysLeuAspGlyCysCysTyrAlaValLysArgIleProIleAsnProAlase 627
Db 1848 ACGTAATGCTCTCGATAGCAGATCTATCGCATCAAGAAG-----ATTAGACATACAGA 1901
QY 627 rArgGlnPheArgArgIleLysGlyGluValThrLeuLeuSerArgLeuHisHisGluAs 647
Db 1902 AGAAAAAGTTATCTACTATATTGAGTGAAGTAATGCTGTTAGCAAGCTTAATCATCAATA 1961
QY 647 nIleValArgTyrTyrAsnAlaTrpIleGluArgHisGluArgProAlaGlyProGlyTh 667

Db 1962 TGTTCGCTTACTATGCTGATGTTAGAGAA- 1995
QY 667 rProProAspSerGlyProLeuAlaLysAspArgAlaAlaArgGlyGlnProAl 687
Db 1995
QY 687 aSerAspThrAspGlyLeuAspSerValGluAlaAlaAlaProProIleLeuSerSe 707
Db 1996
QY 707 rSerValGluTrpSerThrSerGlyGluArgSerAlaSerAlaAlaArgPheProAlaThrG1 727
Db 2010 AAACGTTTTTGAATCACTGATGAGAAAGTGACTTGAC- 2049
QY 727 yProGlySerSerAspAspGluAspGluAspGluHisGlyGlyValPheSerG1 747
Db 2050 -GAATCTCTCTGATTTTGAGGAAATGATTTATTAGATCAAGACGATATTTTAAAAA 2108
QY 747 n- 2109 TAGAACAAATCAGATTTGCGATAATAGTAAGTGGGATTTTCATTCGGGTCA- 756
Db 756 userAspIlePheAspAsn- 767
Db 2166 TCCGGATATGCTTTGAAATAGTCTCGTGATGATGAAATGAAGATCTAGACCATGA 2225
QY 768 SerLysSerGlnAsnGlnAspGluAspCysAsnGluLysAsnGlyCy 783
Db 2226 TACTTCTCGACTCTCTCGAGGAAAGTCAAGATGATGATCAATGAAGAAATCAAGAGATAT 2285
QY 783 shisGlu- 796
Db 2286 CAGAACGTTCCAGAGAGAGAAATTTGTAAACCAGTACTGCTGTAAAGAGAAAG 2345
QY 796 sTyLeuTyrlleGlnMetGluTyrcysGluLysSerThrLeuArgAspThrle- 815
Db 2346 TACGCTTTTATCAATGGAGTACTGTGAAATAGAACGCTATATGTTGATTCATTC 2405
QY 815 pGlnGlyLeuTyrcysAspThrValArgLeuTrpArgLeuPheArgGluIleLeuAspG1 835
Db 2406 TGAAATTTAAATCAACAACTGATGAATATTTGGAGGTATTTTCGACAAATTTTGAAGC 2465
QY 835 yLeuAlaTyrlleHisGluLysGlyMetIleHisArgAspLeuLysProValAsnIlePh 855
Db 2466 ACTGAGTTATATACATCCAGGGTATCATTCATAGGGATCTCGAACCAATGAATATTTT 2525
QY 855 eLeuAspSerAspHisVallyllyleGlyAspPheGlyLeuAlaThrAspHisLeuAl 875
Db 2526 TATAGATCAATCGAGAAATGTAAATCGGTGATTTTGGTTAGCT- 2571
QY 875 aPheSerAlaAspSerLysGlnAspGlnThrGlyAspLeuIleLysSerAsp- 893
Db 2572 -NAGAACCTCATAGATCTCTGGATATATCTTAAGTACAGTATTCACA 2615
QY 894 ProSerGlyHisLeuThrGlyMetValGlyThrAlaLeuTyrcysVal 2615
Db 2616 GAATTTGCCAGGAGCTCGATATAATTAACATCCGCCATTTGTACAGCAATGATTTGTC 2675
QY 909 rProGluValGlnGlySerThrLysSerAlaTyrcysGlnLysValAspLeuPheSerLe 929
Db 2676 TACTGAGTTTATAGTGTACA- 2732
QY 929 uGlyIlePhePheGluMetSerTyrcysHisProMetValThrAlaSerGluArgIlePh 949
Db 2733 TGGAAATCAATTTTGAATGATCTAT- 2789
QY 949 eValLeuAsnGlnLeuArgAspProThrSerProLysPheProGluAspPheAspG1 969
Db 2790 TATTTTGAAGAGTTTACGATCA- 2846
QY 969 yGluHisAlaLysGlnLysSerValIleSerTrpLeuAsnHisAspProAlaLysAr 989

Db 2847 TAAGATGAAAGTTGAAAGAAATTTATAAGGTTACTATAGACCATGATCCCAATAAAG 2906
QY 989 gProThrAlaThrGluLeuLysSerGluLeuLeuProProGlnMetGluGluSe 1009
Db 2907 GCCTGGTGTAGACATTTATAATAGTGTGGCTTCTGTGAAGCATCAGGATGAA- 2964
QY 1009 rGluLeuHisGluValLeuHisThrLeuThrAsnValAspGlyLysAlaTyrcysTh 1029
Db 2965 -GTAATCAAGAGGCTTTTA- 3020
QY 1029 rMetMetAlaGlnIlePheSerGlnArgIleSerProAlaIleAspTyrcysThTyrcys 1049
Db 3021 AGTTTCAGAGAAATTTATTATTAACCA- 3062
QY 1049 rAspIleLeuLysGlyAsnPheSerIleArgThrAlaLys- 3062
Db 3063 TGATATCTATTGATTAAC- 3119
QY 1064 nGlnHisValCysGluThrIleIleArgIlePheLysArgHisGlyAlaValGlnLeuCy 1084
Db 3120 GTCCCAATGACAGAGAGGTAGTTAAATTTTCAGAAACATGGAGAAATTTGAAATAA 3179
QY 1084 sThrProLeuLeuLeuProArgAsnArgGlnIleTyrcysGlnHisAsnGluAlaLeuPh 1104
Db 3180 TGCTCTCCGAGGATTTTTCAGAGGCGCCCATATACGTACGTCAGCAATGTATGAAGT 3239
QY 1104 eMetAspHisSerGlyMetLeuValMetLeuProPheAspLeuArgIleProPheAlaAr 1124
Db 3240 GCTTGACAGAGGCGGTACCGTCTGAGTTACATATGATTTAACTTATCTATGCTAG 3299
QY 1124 gTyrcysValAlaArgAsnLeuLeuAsnLeuLysArgTyrcysIleGluArgValPheAr 1144
Db 3300 GTATCTCTTAAATAATCAAGTCTGATTTCTAAGCAATATAGTACGACGACGTTTACCG 3359
QY 1144 gProArgLysLeuAspArg- 1162
Db 3360 ACCTCTGATCATTCAGGTCAAGTTTGGAACTAGAAAGTTTGGTGAATTCGATTCGA 3419
QY 1162 pIleValThr- 1181
Db 3420 CATAAATTTCAAAATCTCTCTCAGAGTCAGATTTTATGATGACAGAAAGCTTGAATAT 3479
QY 1181 eTyrcysGluIleGlnGluPheProAlaLeuGlnArgAsnTyrcysIleTyrcysLeuAs 1201
Db 3480 CGATGAATATTAACCGTATTTCTCTGATTTGAGAAACAAACACACTTTTTCATATTA 3539
QY 1201 nHisThrMetLeuLeuAlaIleLeuLeuHisCysGlyIleProGluAspLys- 1219
Db 3540 TCATGCTGATATTTTGAGAGTGTTTTCAACTTTTCAAAATATTTGATAAGCCCAAGGCC 3599
QY 1220 LeuSerGlnValTyrcysIleLeuTyrcysIleLeuTyrcysIleValThrGluLys 1234
Db 3600 TCTAGTTTCAGAAATGTTGTCGCAAGTAGGCTTT- 3647
QY 1234 sLeuThrArgArgGluValGluAlaLysPheCysAsnLeuSerLeuSerSerAsnSerLe 1254
Db 3648 GGAAGTAAAGATGAACATAAGCGCAA- 3698
QY 1254 uCysArgLeuTyrcysPheIleGluGlnLysGlyAspLeuGlnAspLeuMetProThrI 1274
Db 3699 GAATGATTTGGAGTTATTT- 3755
QY 1274 eAsnSerLeuIleLysGlnLysThrGlyIleAlaGlnLeuValLysTyrcysGlyLysAs 1294
Db 3756 GTATAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3812
QY 1294 pLeuGluValValGlyLeuLeuLysLysLysLysLysLysLysLysLysLysLysLys 1314
Db 3813 TATATCAAGAGTCTCTGATTTTACCTTAAACCTTAGAAGTTGCAAGAAATCTTGTGATTC 3872
QY 1314 nLeuGlyLeuValTyrcysValGlnGlnHisAsnGlyIleIlePheGlnPheValAlaPh 1334
Db 3873 TCCTTTGTAGTAACTAATAGCGCTTTTTCAGAAAGGAGGTATCATGTTTTCAGCTTTA 3932

Db 3172 TTCATGGAACAAAC-----TACTCCATAAGTGGACATCTCTTTAGGCTTGA 3222
 QY 932 lePhePheGluMetSerTyrHisProMetValThrAlaSerGluArgIlePheValLeuA 952
 Db 3223 TTTGTTTGAATCTCTTAC---CCATTCAGACCCAGATGGAACGAGTCCGATTTAA 3279
 QY 952 snGlnLeuArgAspProThrSerProLysPheProGluAspPheAspAspGlyGluHisA 972
 Db 3280 CTGATGTGAGA-----AATCTCAAGTTTCTCTACTGTTCACCTCAG---AAATATC 3327
 QY 972 laLysGlnLysSerValIleSerTrpLeuLeuAsnHisaspProAlaLysArgProThrA 992
 Db 3328 CCCAAGAGCATATGATGGTTCAAGACATGCTCTCCATCCCCAGGAGCGCTGAAG 3387
 QY 992 laThrGluLeuLeuLysSer-----GluLeuLeuProProProGlnMetGluGluS 1009
 Db 3388 CCACAGACATCAATGAAATGCCATATTTGAGAACTTGAGATTCCCGG-GAAACGGTT 3446
 QY 1009 erGluLeuHisGluValLeuHisThrLeuThrAsnValAspGlyLysAlaTyrArgT 1029
 Db 3447 CTGAGACAGCGTCCCGCTCCATGAGTTTCATCTGGAAC-----AAAACATTCCAGA 3497
 QY 1029 hrMetMetAlaGlnIlePheSerGln 1037
 Db 3498 CA-----GCCAGCTGCTCGTACAG 3517

RESULT 9

US-10-197-666A-101
 ; Sequence 101, Application US/10197666A
 ; Publication No. US2003092037A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ASAHI KASEI KABUSIKI KAISYA
 ; FILE REFERENCE: PH-1548US
 ; CURRENT APPLICATION NUMBER: US/10/197,666A
 ; PRIOR FILING DATE: 2002-11-18
 ; PRIOR APPLICATION NUMBER: JP 2001-218204
 ; PRIOR FILING DATE: 2001-07-18
 ; PRIOR APPLICATION NUMBER: JP 2001-263450
 ; PRIOR FILING DATE: 2001-08-31
 ; PRIOR APPLICATION NUMBER: JP 2002-012176
 ; PRIOR FILING DATE: 2002-01-21
 ; PRIOR APPLICATION NUMBER: US 60/305,884
 ; PRIOR FILING DATE: 2001-07-18
 ; PRIOR APPLICATION NUMBER: US 60/316,304
 ; PRIOR FILING DATE: 2001-09-04
 ; PRIOR APPLICATION NUMBER: US 60/350,027
 ; PRIOR FILING DATE: 2002-01-23
 ; NUMBER OF SEQ ID NOS: 156
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 101
 ; LENGTH: 4391
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (72)..(1961)
 US-10-197-666A-101

Alignment Scores:
 Pred. No.: 1,47e-36 Length: 4391
 Score: 479.00 Matches: 290
 Percent Similarity: 36.52% Conservative: 142
 Best Local Similarity: 24.51% Mismatches: 392
 Query Match: 5.61% Indels: 361
 DB: 9 Gaps: 55

US-09-515-806A-2 (1-1649) x US-10-197-666A-101 (1-4391)

QY 550 GlnSerProGluAspSerGlyGlnAspTyrValGluThrValIleProSerAsnArg 569
 Db 456 AGGTCTGTAAGAGAGAGAGTTCGTGAGGATCTTCTGAGGATATTTCTCTGATCCAGAA 515

QY 570 LeuProSerAlaIlePhePheSerGluThrGlnArgGlnPheSerArgTyrPheIleGlu 589
 Db 516 ATCAGATCAAGGAAGTAGCTTTGGGAAGCACAACT-----TCAGTTTACTTAATGAA 569
 QY 590 PheGluGluLeuGlnLeuLeuGlyLysGlyAlaPheGlyAlaValIleLysValGlnAsn 609
 Db 570 TTTGAAGAATCTTCCATCTTAGGAAAGGTGATACGGAAGAGATATACAAGGTCCAGGAAT 629
 QY 610 LysLeuAspGlyCysCysTyrAlaValLysArgIlePheProIleAsnProAlaSerArgGln 629
 Db 630 AAATTAGATGGTCAGTATTATGCAATAAAAAAACTCTGATTAAAGGTGCAACTAAACA 689
 QY 630 Phe---ArgArgIleLysGlyGluValThrLeuLeuSerArgLeuHisHisGluAsnIle 648
 Db 690 GTTTGCATGAAGTCTTACCGGAAGTGAAGTGTGGCAGGTCTTTCAGCACCCCAATATT 749
 QY 649 ValArgTyrTyrAsnAlaTrpIleGluArgHisGluArgProAlaGlyProGlyThrPro 668
 Db 750 GTTGGCTATCACACCGCTGGATAGAA---CATGTTTCATGTGATTCAGCCA----- 797
 QY 669 ProProAspSerGlyProLeuAlaLysAspAspArgAlaAlaArgGlyGlnProAla--- 687
 Db 798 -----CGAGCAGACAGAGCTGCCATTGAGTTGCCATCTCTG 833
 QY 688 -----SerAspThrAsp 691
 Db 834 GAAGTGTCTCCGACCAGGAAGAGCAGACAGCAATGTGCTTTAAAAATGATGAAAGT 893
 QY 692 GlyLeuAspSerValGluAlaAlaProProIleLeuSerSerVal---Glu 710
 Db 894 AGCAGCTATCCATTATCTTGTGAGCCGCCCAAGAAAAAAGAAAAACCTTTGAGAA 953
 QY 711 TrpSerThrGlyGluArgSerAlaSerAlaArgPheProAla-----ThrGlyPro 728
 Db 954 TCTGACACTGAAATCAGAAATCAAGTCCGTGAAGTACACCACTAATTTAGTCATAAGA 1013
 QY 729 GlySerSerAspGluAspAspGluAspGluHisGlyGlyValPheSerGlnSer 748
 Db 1014 GAATCTGTTGAACTTGTGACCTCGACCTCGAGAAATGGCTTGGCTGGTTGCT 1073
 QY 749 PheLeuProAlaSerAspSerGluSerAspIlePheAspAsnGluAspGluAsnSer 768
 Db 1074 -----GCCAGTTCAATTGTGGAACAGCAGCTGCCACTCAGCGCTAATTTCCACCCTAGAG 1127
 QY 769 LysSerGlnAsnGlnAspGluAspCysAsnGluLysAsnGlyCysHisGluSerGlnPro 788
 Db 1128 GAGAGTTTCATCTCCACCGAAGAAATCTTCCGAAGAAATGTCAACTTTTGGGTGAG--- 1184
 QY 789 SerValThrThrGluAlaValHisTyr-----LeuTyrIleGlnMetGluTyrCysGlu 806
 Db 1185 -----ACAGAGCAGACAGTACCACCTGATGCTGCACATCCAGATGCACTGTGTGAG 1235
 QY 807 LysSerThrLeu-----ArgAspThrIleAspGln 816
 Db 1236 CTCTCGCTGTGGGATTGGATAGTCGAGAGAAACAAAGCGGGCCGGAGTAGTGTGACAG 1295
 QY 817 GlyLeu-----TyrArgAspThrValArgLeuTrpArgLeuPheArgGluIleLeuAsp 834
 Db 1296 TCTGCTGCTCTTATGTTATGGCAATGTTGCCAACAAAAATTTTCAAGAAATGGTAGAA 1355
 QY 835 GlyLeuAlaTyrIleHisGluLysGlyMetIleHisArgAspLeuLysProValAsnIle 854
 Db 1356 GGTGTGTTTTACATACATAAATCGGAATTTGTCACCGAGATCTGAAGCCCAAGAAATATT 1415
 QY 855 PheLeuAspSer---AspAspHisValLysIleGlyAspPheGlyLeuAla---ThrAsp 872
 Db 1416 TTTCTTCATGCCCTGATCAGCAAGTAAAAATAGGAGACTTTGCTGTGGCTCCACAGAC 1475
 QY 873 HisLeuAlaPheSerAlaAspSerLysGlnAspGlnThrGlyAspLeuIleLysSer 892
 Db 1476 ATCCTA-----CAGAGAACACAGACTGGACCAACAGAAACCGGAAGAGA 1520

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893 AspProSerGlyHisLeuThrGlyMetValGlyThrAlaLeuTyrValSerProGlu--- 911
 1521 ACACCAACA---CAT---ACGTCAGAGTGGTACTGTGTACGCTTACCCGCAACAG 1574
 912 ValGlnGlySerThrLysSerAlaTyrAsnGlnLysValAspLeuPheSerLeuGlyIle 931
 1575 TTGGAAGGA---TCTGAGTATGATGCCAAGTCAGATATGTACAGCTTGGGTGTG 1625
 932 IlePhePheGluMetSerTyrHisProMetValThrAlaSerGluArgIlePheValLeu 951
 1626 GTCCTGCTAGACTC---TTTCAGCCGTTTGGAAACAGAAATGGAGCAGAGAATTCCTA 1682
 952 AsnGlnLeuArgAspProThrSerProLysPheProGluAspPheAspAspGlyGluHis 971
 1683 ACAGGTTTAAAG---ACTGGTCAGTTGCCGGAATCCCTCCGTA---AGGTGT 1730
 972 AlaLysGlnLysSerValIleSerTrpLeuLeuAsnHisAspProAlaLysArgProThr 991
 1731 CCAGTCAGCCCAAGTATATCCAGCAGCTTAACGAGAAGAACTCATCGCAGAGACCATCT 1790
 992 AlaThrGluLeuLeuLysSerGluLeu----- 1000
 1791 GCCATTGAGTGTGCGAGAGTGAACCTTTCCAAAATTCGGAATGTTAACTCACCTCA 1850
 1001 -----LeuProProGlnMetGluSerGluLeuHisGluValLeuHisHis 1017
 1851 CAGATGAAGATATAGACGCAAGAAAGAAATTTGCAGAACTAAAGAACGAGCTAAACCTC 1910
 1018 ThrLeuThrAsnVal-----AspGlyLys----- 1025
 1911 CTTTCTCAAGACAAAGGGGTGAGGAGTACGGAAGGATGGGGGCGTGGGATGAAGTGG 1970
 1026 -----AlaTyr-ArgThrMetMet 1031
 1971 ACTTAACCTTTAAGGTAGTTAACTGGAATGTAATTTTAACTTTATTTAGGGTATAGTT 2030
 1031 tAlaGlnIlePheSerGlnArgIleSerProAlaIleAspTyrThrTyrAspSerAsp--- 1050
 2031 GGTACAATGCTTCGTTGTTATTTAGTAAAGCCTTTTACAGACTGTTTAAAGATGTCAGAGTG 2090
 1051 -----IleLeuLysGlyAsnPheSerIle 1058
 2091 CCCCAGGTGGGTCCTTCCCTTCCCTCCGCCCCCAAGCTCCTTTCTGTAATTTCTACCT 2150
 1058 eArg-----ThrAlaLysMetGlnGlnHisValCysGlnThrIleIle 1072
 2151 TAAATATTAAACCATATGCTAGTCTCTGGAAGTAACTAAAGAACTTGGACCTCATCTCAATTAT 2210
 1072 eArgIlePheLysArgHisGlyAlaValGlnLeuCysThrProLeuLeuLeuProArgAs 1092
 2211 TTTCTCCTTT-----CAACTCTGTTGACCTCTGCTGGTCTTCCTC 2252
 1092 nArgGlnIleTyrGluHisAsnGluAlaAlaLeuPheMetAspHisSerGlyMetLeuVa 1112
 2253 TAGAAGGTTCTACCGCAGAAATTTGATGT----- 2280
 1112 lMetLeuProPheAspLeuArgIleProPheAlaArgTyrValAlaArgAsnAsnIleLe 1132
 2281 -GTGCTCCCT-----GCCCTCTGCTACGCGCCAA----- 2307
 1132 uAsnLeuLysArgTyrCysIleGluArgValPheArgProArgLysLeuAspArgPheHi 1152
 2308 -----GCCCGGGCCTGCACATACCTCA----- 2328
 1152 sProLysGluLeuLeuGluCys---AlaPheAspIleValThrSerThrThrAsnSerPh 1171
 2329 -----CTGACCTGTTCCAGTTTTCAGACCTGCCAGTCTTCCTG---CCCTT 2372
 1171 eLeuProThrAlaGluIleIleTyr----- 1179
 2373 TCACATGCGAGCTGAAGTTTATTAACCTGAAGAGCGGCTCATCATTTCTTCCTGCTCC 2432
 1180 -----ThrIleTyrGluIleIleG 1186

2433 AAACCTTCGTGCTGCTCTTAAGATAAAGCTCAACTTCTTAACAGTGTACAGTGTG--- 2487
 1186 nGluPhePro-----AlaLeuGlnGluArgAsnTyrSerIleTyrLeuAsnHi 1202
 2488 -CAACTTCCAACCTTTTATCTCTCTCCACCTTCAGCTTTAGCGTCAATTCCAAACA 2546
 1202 sThrMet----- 1206
 2547 CACCTTTGCAAGCTTTGTACTCCGACCCAGATGATCTCCAGGCGAGCTCAGATCTCTT 2606
 1206 uLysAlaIleLeuLeuHisCysGlyIleProGluAspLysLeuSerGlnValTyrIleIle 1226
 2607 TCCTGGCTTTGCCCTGCACCTGT----- 2628
 1226 eLeuTyrAspAlaValThrGluLysLeuThrArgGluValGluAlaLysPheCysAs 1246
 2629 -----TCCCGGTACTCTCTCTTTATGTAGCACTCCGACCAATCTGTAT 2681
 1246 nLeuSerLeuSerSerAsnSerLeuCysArgLeuTyrLysPheIleGluGlnLysGlyAs 1266
 2682 A---TCCCTCAGAGCGAGCTCTGAT-GAATTGGTT---TTTGAATCCCAAGAGGTC 2734
 1266 pLeuGlnAspLeu----- 1270
 2735 TGCCATGGAGTTGGCAGTCATCAGCGTAGTGGCGTATGATTTTGCTGAATTTTAAATAA 2794
 1271 -MetProThrIleAsnSerLeu----- 1277
 2795 AATGAACCATTAATTTACATGATGCTTTTATGACACTTTGACAACTGGCGCTAAATAAAA 2854
 1278 ----- 1278
 2855 AGACTCTGACTCTAATACAAAGTCCCTTACTGATTAATAGGCATGAAGAGCACCATCTT 2914
 1278 eLysGlnLysThrGlyIleAlaGlnLeuValLysTyrGlyLeuLysAspLeuGluVa 1298
 2915 AAAATCTAAA-----CCCTTTAAATCATGTTACGGC---AATTCACTTAAGGAGCT 2962
 1298 lValGlyLeuLeuLysLys-----LeuG 1306
 2963 TGAGGCGCGTGTAAAGAGCGCAGGTTTTTCAAGACCTCATCCACTCTGCACATTGG 3022
 1306 yLeLysLeuGlnValLeuIleAsnLeuGlyLeuValTyrLysValGlnGlnHisAsnG 1326
 3023 CTGGCACTGTCACACTGCAGCCTCCGATCTGTGGAGTACAGACACAGCACAC 3077
 1326 yIleIlePheGlnPheValAlaPheIleLysArgGlnArgAlaValProGluIleLe 1346
 3078 -----GTCTGCTACGGTGAGTTTCATCCACGAGCCCAAGGCTCTTCCCAAGAGCAG 3130
 1346 uAlaAlaGlyGly-Arg-----TyrAspLeuLeuIleProGlnPheArgGlyProG 1363
 3131 AGTTCATGAGCGGAAACACAGCGCTTTTCTTACTGTCTCTCTCTTAACTGAAAAA 3190
 1363 lAlaLeuGlyProValProThrAlaIleGlyValSerIleAlaIleAspLysIle-Ser 1382
 3191 TCGCA-----ATATCTACCAGATCTATAGGGTTGCGTTGACAGCATTATGCT 3241
 1383 AlaAlaValLeuAsnMetGluLysSerValThrIleSerSerCysAspLeuLeuVal--- 1401
 3242 TCTGCCCAACAGAGAGAACAAAGACGTG-----CAATGTTCTCTCTCGCTTCGA 3292
 1402 -----ValSerValGlnMetSerMetSerArgAlaIleAsnLeuThrGlnLysLeu 1419
 3293 TGGGGCACATCTCTGGATGCTGAATTTTCATCTTCGCTTCGCGACCTGAAAAAGAAAAC 3352
 1420 TrpThrAlaGlyIleThr-----AlaGluIleMetTyrAspTrpSerGlnSer 1435
 3353 AGCCAGGTAGCATCACACAGCAGCCCTGAGGGAAGTACTCGCAGCTGAGGGAAGGGA 3412
 1436 GlnGluGluGlnGlnLutyrCysArgHisHisGluIleThrTyrValAlaLeuValSer 1455

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Alignment Scores:
Pred. No.: 2,97e-36 Length: 4448
Score: 476.00 Matches: 291
Percent Similarity: 36.68% Conservative: 143
Best Local Similarity: 24.60% Mismatches: 390
Query Match: 5.57% Indels: 361
DB: 9 Gaps: 56

US-09-515-806A-2 (1-1649) x US-10-198-846-12737 (1-4448)

QY 550 GlnSerProGluAspSerGlyGlnAspTy+ValGluThrValIleProSerAsnArg 569
Db 3928 AGGTCGTCTAAAGAGAGATTGTCAGAGTCCTGTGAGAGATATTCTCGTATCCAGAAA 3869
QY 570 LeuProSerAlaAlaPhePheSerGluThrGlnArgGlnPheSerArgTy+PheIleGlu 589
Db 3868 ATCAGATCAAGCGGAAGTAGCCTTGGAAAGCACAAACT-----TCACGTTACTTAAATGAA 3815
QY 590 PheGluGluLeuGlnLeuLeuGlyIleGlyAlaPheGlyAlaValIleLysValGlnAsn 609
Db 3814 TTTGAGNACTTGCCATCTTTAGGAAAGGTGGATACGGAAGATATACAAGGTCAGGAAT 3755
QY 610 LysLeuAspGlyCysCysTyrAlaValLysArgIleProIleAsnProAlaSerArgGln 629
Db 3754 AAATTAGATGTCAGTATTATGCAATATAAAAAAATCTCGATTAAAGGTCGAACATAAACA 3695
QY 630 Phe---ArgArgIleLysGlyGluValThrLeuLeuSerArgLeuHisHisGluAsnIle 648
Db 3694 GTTTGCATGAAGTCCTCGGGAAGTGAAGGTGCTGGCAGGCTCTTCAGCACCAATATT 3635

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Thu Jun 12 14:34:05 2003

Db 1869 ATAATAGAACAGAGAAATTTGAAGAACTA 1901

RESULT 12

US-09-799-875-18

; Sequence 18, Application US/09799875

; Patent No. US20020034780A1

GENERAL INFORMATION:

; APPLICANT: Meyers, Rachel

; APPLICANT: Kapeller-Libermann, Rosana

; APPLICANT: Williamson, Mark

; TITLE OF INVENTION: No. US20020034780A1 Human Protein Kinases and Uses

; FILE REFERENCE: 35800/209996

; CURRENT APPLICATION NUMBER: US/09/799, 875

; CURRENT FILING DATE: 2001-03-06

; PRIOR APPLICATION NUMBER: 60/182,059

; PRIOR FILING DATE: 2000-02-11

; PRIOR APPLICATION NUMBER: 09/659,287

; PRIOR FILING DATE: 2000-09-12

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 18

; LENGTH: 1887

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-799-875-18

Alignment Scores:
Pred. No.: 2,77e-36 Length: 1887
Score: 470.00 Matches: 161
Percent Similarity: 47.03% Conservative: 69
Best Local Similarity: 32.92% Mismatches: 185
Query Match: 5.50% Indels: 74
Gaps: 22

US-09-515-806A-2 (1-1649) x US-09-799-875-18 (1-1887)

QY 550 GlnSerProGluAaspSerGlyGlnAspTyrValGluThrValIleProSerAsnArg 569
Db 385 AGGCTCTGTAAGAGAGAGATTCGTCAGGATCCTTGTGAGGATATTTCTCGTATCCAGAAA 444
QY 570 LeuProSerAlaAlaPhePheSerGluThrGlnArgGlnPheSerArgTyrPheIleGlu 589
Db 445 ATCAGATCAGGAAGTAGCTTGAAGCACAACACT-----TCACGTTACTTAAATGAA 498
QY 590 PheGluGluLeuGlnLeuGlyGlyAlaPheGlyAlaPheGlyAlaValIleLysValGlnAsn 609
Db 499 TTTGAAGAACTTGCCATCTTAGGAAAGGTGGATACGGAAGAGATATACAGGTTCAGGAAT 558
QY 610 LysLeuAspGlyCysCysTyrAlaValIleLysValGlnAsn 629
Db 559 AAATTAGATGGTCAGTATTATGCAATAAATAAATCCTGATTAAAGGTGCAACTTAAACA 618
QY 630 Phe---ArgArgIleLysGlyGluValThrLeuLeuSerArgLeuHisHisGluAsnIle 648
Db 619 GTTTGGATGAAGTCTCTACGGAAGTGAAGTGGCTGGCAGGTCTTCAGCACCCCAATATT 678
QY 649 ValArgTyrThrAsnAlaTrpIleGluArgHisGluArgProAlaGlyProGlyThrPro 668
Db 679 GTTGGCTATCACACCGGTGGATAGAA---CATGTTTCATGTTGATTCAGCCA----- 726
QY 669 ProProAspSerGlyProLeuAlaLysAspAspArgAlaAlaArgGlyGlnProAla--- 687
Db 727 -----CGAGACAGAGCTGTCATTTGAGTTGCTGCTCTCTG 759
QY 688 -----SerAspThrAsp 691
Db 760 GAAGTGTCTCCGACCAAG 819
QY 692 GlyLeuAspSerValGluAlaAlaAlaProProProIleLeuSerSerVal---Glu 710
Db 820 AGCAGCTCATCCATTATCTTTGCTGAGCCACCCCAAGAAAAAGAAAAAGAAAAAGAAAAAG 879

QY 711 TrpSerThrSerGlyGluArgSerAlaSerAlaArgPheProAla-----ThrGlyPro 728
Db 880 TCTGACACTGAAATCAGAAATACAGTGGTCAAGTACACACCAATTTAGCTATAAGA 939
QY 729 GlySerSerAspAspGluAspAspGluAspGluHisGlyGlyValPheSerGlnSer 748
Db 940 GAATCTGTTGAATGAGTCCACCTGGAGCTCCAGGAAATGGCTTGCTGGTTGCT 999
QY 749 PheLeuProAlaSerAspSerGluSerAspIlePheAspAsnGluAspGluAsnSer 768
Db 1000 -----GCCAGTTTCAATTTGGAAACACGACCTCCACTCAGCGCTAATTCACCACTAGAG 1053
QY 769 LysSerGlnAsnGlnAspGluAspCysAsnGluLysAsnGlyCysHisGluSerGluPro 788
Db 1054 GAGAGTTTTCACATCCACGGAAGATCTTCGAAAGAAATTCACATTTTGGGTGAG--- 1110
QY 789 SerValThrThrGluAlaValHisTyr-----LeuTyrIleGlnMetGluTyrCysGlu 806
Db 1111 -----ACAGAGGACAGTACCACTGATGCTGCATCCAGATGCAGCTGTGTGAG 1161
QY 807 LysSerThrLeu-----ArgAspThrIleAspGln 816
Db 1162 CTCTCGCTGGATTGGATAGTCGAGAGAAACAAGCGCGCGGAGTATGTGGAGAG 1221
QY 817 GlyLeu-----TyrArgAspThrValArgLeuTrpArgLeuPheArgGluIleLeuAsp 834
Db 1222 TCTGCCTGCTCTTATGTTATGCGCAATGTTGCAACAAAAATTTTCAAGAAATGCTAGAA 1281
QY 835 GlyLeuAlaTyrIleHisGluLysGlyMetIleHisArgAspLeuLysProValAsnIle 854
Db 1282 GGTGTGTTTATACATATAACATGGAAATTTGTGACCGAGATCTGAAGCCCAAGAAATATT 1341
QY 855 PheLeuAspSer---AspAspHisValIleGlyAspPheGlyLeuAla---ThrAsp 872
Db 1342 TTTCTTCATGGCCCTGATCAGCAAGTAAATAATAGGAGACTTTTGTCTGCGCTGCACAGAC 1401
QY 873 HisLeuAlaPheSerAlaAspSerLysGlnAspAspGlnThrGlyAspLeuIleLysSer 892
Db 1402 ATCTCA-----CAGAGAGAACACAGACTGGACCAACAGAAACGGGAAGAGA 1446
QY 893 AspProSerGlyHisLeuThrGlyMetValGlyThrAlaLeuTyrValSerProGlu--- 911
Db 1447 ACACCAACA---CAT---ACGTCACAGAGTGGGTACTTGTCTGTACGCTTCAACCCGACAG 1500
QY 912 ValGlnGlySerThrLysSerAlaTyrAsnGlnLysValAspLeuPheSerLeuGlyIle 931
Db 1501 TTGAAGAA-----TCTGATGATGATGCAAGTCAAGTATGTACAGTCTGGGTGTG 1551
QY 932 IlePhePheGluMetSerTyrHisProMetValThrAlaSerGluArgIlePheValLeu 951
Db 1552 GTCCTGCTAGAGTCT---TTTTCAGCCCTTTGGAAACAGAAATGGAGCGAGCAGAGTTCTTA 1608
QY 952 AsnGlnLeuArgAspProThrSerProLysPheProGluAspPheAspAspGlyGluHis 971
Db 1609 ACAGGTTTAAAGA-----ACTGTGTCAGTTCGCGGAATCCCTCCGTAAA---AGGTGT 1656
QY 972 AlaLysGlnLysSerValIleSerTrpLeuLeuAsnHisAspProAlaLysArgProThr 991
Db 1657 CCGGTGCAAGCAAGTATATATCCAGCACTTAACGAGAAAGAACTATCCGAGAGCACTCT 1716
QY 992 AlaThrGluLeuLeuLysSerGluLeu 1000
Db 1717 GCCATTGCTGCTGACAGTGAACCTT 1743

RESULT 13

US-10-197-666A-103

; Sequence 103, Application US/10197666A

; Publication No. US20030092037A1

GENERAL INFORMATION:

; APPLICANT: ASAHU KASEI KASUYUKI KAISYA

; TITLE OF INVENTION: Elkl phosphorylation related gene

; FILE REFERENCE: PH-154805

; CURRENT APPLICATION NUMBER: US/10/197,666A

; CURRENT FILING DATE: 2002-11-18
 ; PRIOR APPLICATION NUMBER: JP 2001-218204
 ; PRIOR FILING DATE: 2001-07-18
 ; PRIOR APPLICATION NUMBER: JP 2001-263450
 ; PRIOR FILING DATE: 2001-08-31
 ; PRIOR APPLICATION NUMBER: JP 2002-012176
 ; PRIOR FILING DATE: 2002-01-21
 ; PRIOR APPLICATION NUMBER: US 60/305,884
 ; PRIOR FILING DATE: 2001-07-18
 ; PRIOR APPLICATION NUMBER: US 60/316,304
 ; PRIOR FILING DATE: 2001-09-04
 ; PRIOR APPLICATION NUMBER: US 60/350,027
 ; PRIOR FILING DATE: 2002-01-23
 ; NUMBER OF SEQ ID NOS: 156
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 103
 ; LENGTH: 2844
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (52)..(1938)
 ; US-10-197-666A-103

Alignment Scores:
 Pred. No.: 5,51e-36 Length: 2844
 Score: 470.00 Matches: 161
 Percent Similarity: 47.03% Conservative: 69
 Best Local Similarity: 32.92% Mismatches: 185
 Query Match: 5.50% Indels: 74
 DB: 9 Gaps: 22

US-09-515-806A-2 (1-1649) x US-10-197-666A-103 (1-2844)

QY 550 GlnSerProGluAspSerGlyGlyGlnAspTyrValGluThrValIleProSerAsnArg 569
 Db 436 AGGTCCTCTAAAGAGAGAGTCTCGAGGATCTTGTGAGGATATTTCTCGTATCCAGAAA 495
 QY 570 LeuProSerAlaAlaPheSerGluThrGlnArgGlnPheSerArgTyrPheIleGlu 589
 Db 496 ATCAGATCAGGGAAGTACGCTTGAAGCACAACCT-----TCAGTTTCTTAATATGAA 549
 QY 590 PheGluGluLeuGlnLeuGlyGlyGlyAlaPheGlyAlaValIleLysValGlnAsn 609
 Db 550 TTGTAAGAACTTGCCATCTTAGAAGAGTGTGATACGGAAGATATACAGGTGAGGAT 609
 QY 610 LysLeuAspGlyCysCysTyrAlaValIleValIleProIleAsnProAlaSerArgGln 629
 Db 610 AATATAGATGTCAGTATTATGCAATAAAAAATCCTGATTAGGGTGCACATAAACA 669
 QY 630 Phe---ArgArgIleLysGlyGluValThrLeuSerArgLeuHisGluAsnIle 648
 Db 670 GTTTCATGAAGTCTCTACGGAAGTGAAGTGTGCGAGGCTTTCAGCACCCCAATATT 729
 QY 649 ValArgTyrTyrAsnAlaTyrIleGluArgHisGluArgProAlaGlyProGlyThrPro 668
 Db 730 GTTGCTATCACCGGCTGATAGAA---CATGTTTCATGTCATTCAGCCA----- 777
 QY 669 ProProAspSerGlyProLeuAlaLysAspAspArgAlaAlaArgGlyGlnProAla--- 687
 Db 778 -----CGAGACAGAGTGCATTTAGTTGCTCCATCTCTG 810
 QY 688 -----SerAspThrAsp 691
 Db 811 GAAGTGTCTCCAGCAGGAGAGAGAGCAATGTGTGTTAAATGATGAAAGT 870
 QY 692 GlyLeuAspSerValGluAlaAlaProProIleLeuSerSerVal---Glu 710
 Db 871 AGCAGCTCATCTTATCTTCTGAGCCCAACCCAGAAAAAAGAAACCTTTGAGAA 930
 QY 711 TrpSerThrSerGlyGluArgSerAlaAlaPheProAla-----ThrGlyPro 728
 Db 931 TCTGACACTGAAATATCAAGAAATCAAGTCTGTAAGTACACCACTATTAGTCATAAGA 990

QY 729 GlySerSerAspAspGluAspAspGluAspGluHisGlyGlyValPheSerGlnSer 748
 Db 991 GAATCTGTGATCTGAGTCCAGCCCTGAGCTCCAGGAAAAATGCTTGGCTGGTTGCT 1050
 QY 749 PheLeuProAlaSerAspSerGluSerAspIlePheAspAsnGluAspGluAsnSer 768
 Db 1051 -----GCCAGTTTCAATTGTGGAACAGCAGCTGCCACTCAGCGCTAATTTCACCATAGAG 1104
 QY 769 LysSerGlnAsnGlnAspGluAspCysAsnGluLysAsnGlyCysHisGluSerGluPro 788
 Db 1105 GAGAGTTTTCATCCACCGAAGAAATTTCCGAAGAAATGTCAACTTTTGGGTGAG--- 1161
 QY 789 SerValThrThrGluAlaValHisTyr-----LeuTyrIleGlnMetGluTyrCysGlu 806
 Db 1162 -----ACAGAGGCACAGTACCACCTGATGCTGCACATCCAGATGCTGTCAG 1212
 QY 807 LysSerThrLeu-----ArgAspThrIleAspGln 816
 Db 1213 CTCTCGCTGGGATTTGATAGTCGAGAGAAACAGCGGGCGGAGTATGTGACGAG 1272
 QY 817 GlyLeu-----TyrArgAspThrValArgLeuTyrPheArgLeuPheArgGluIleLeuAsp 834
 Db 1273 TCTGCTGTCTTATGTTATGTCACAAAAATTTTCAAGAAATTTGGTAGAA 1332
 QY 835 GlyLeuAlaTyrIleHisGluLysGlyMetIleHisArgAspLeuLysProValAsnIle 854
 Db 1333 GGTGTGTTTACATACATACATGGAATTTGTCGCGAGATCTGAAGCCAGAAATATT 1392
 QY 855 PheLeuAspSer---AspAspHisValLysIleGlyAspPheGlyLeuAla---ThrAsp 872
 Db 1393 TTTCTTATGTCCTGATGATGCAAGTAAAAATAGGAGACTTTTGGTCTGCGCTGCACAGAC 1452
 QY 873 HisLeuAlaPheSerAlaAspSerLysGlnAspAspGlnThrGlyAspLeuIleLysSer 892
 Db 1453 ATCCTA-----CAGAAGAACACAGACTGACCAACAGAAACGGGAAGAGA 1497
 QY 893 AspProSerGlyHisLeuThrGlyMetValGlyThrAlaLeuTyrValSerProGlu--- 911
 Db 1498 ACACCAACA---CAT---ACGTCCAGAGTGGGTACTTCTCTGTACGCTTACCCGGAACAG 1551
 QY 912 ValGlnGlySerThrLysSerAlaTyrAsnGlnLysValAspLeuPheSerLeuGlyIle 931
 Db 1552 TTGGAAGGA-----TCTGAGTATGATGCCAAGTCAGATATGTACAGCTTGGGTGTG 1602
 QY 932 IlePhePheGluMetSerTyrHisProMetValThrAlaSerGluArgIlePheValLeu 951
 Db 1603 GTCTGCTAGAGCTC---TTTCAGCGCTTTTGAACAGAAATGAGCGAGCAGAGTCTTA 1659
 QY 952 AsnGlnLeuArgAspProThrSerProLysPheProGluAspPheAspAspGlyGluHis 971
 Db 1660 ACAGGTTTAAAG-----ACTGTGTCAGTCCCGGAATCCCTCCGTAAA---AGGTCT 1707
 QY 972 AlaLysGlnLysSerValIleSerTrpLeuLeuAsnHisAspProAlaLysArgProThr 991
 Db 1708 CCAGTGCAGCAAGTATATCCAGCACTTAACGAGAAGGAACCTCATCGCAGAGACCATCT 1767
 QY 992 AlaThrGluLeuLysSerGluLeu 1000
 Db 1768 GCCATTGCTGTCAGAGTGAACCTT 1794

RESULT 14

; US-09-799-875-16
 ; Sequence 16 Application US/09799875
 ; Patent No. US20020034780A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Meyers, Rachel
 ; APPLICANT: Kapeller-Libermann, Rosana
 ; APPLICANT: Williamson, Mark
 ; TITLE OF INVENTION: No. US20020034780A1el Human Protein Kinases and Uses
 ; FILE REFERENCE: Therefor
 ; FILE REFERENCE: 35800/209996
 ; CURRENT APPLICATION NUMBER: US/09/799,875

us-09-515-806a-2.rnpb

Thu Jun 12 14:34:05 2003

; CURRENT FILING DATE: 2001-03-06
 ; PRIOR APPLICATION NUMBER: 60/182,059
 ; PRIOR FILING DATE: 2000-02-11
 ; PRIOR APPLICATION NUMBER: 09/659,287
 ; PRIOR FILING DATE: 2000-09-12
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 16
 ; LENGTH: 2870
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (114)...(2000)
 ; US-09-799-875-16

Alignment Scores:
 Pred. No.: 2870
 Score: 5.6e-36
 Percent Similarity: 47.03%
 Best Local Similarity: 32.92%
 Query Match: 5.50%
 DB: 10

US-09-515-806A-2 (1-1649) x US-09-799-875-16 (1-2870)
 QY 550 GlnSerProGluAspSerGlyGlnAspTyrValGluThrValIleProSerAsnArg 569
 Db 498 AGGTCTGTAAAGAGAGAGATTCGTCAGGATCCTTGTGAGGATATTTCTCGTATCCAGAA 557
 QY 570 LeuProSerAlaAlaPheSerGluThrGlnArgGlnPheSerArgTyrPheLeuGlu 589
 Db 558 ATCAGATCAAGGAGAGATTCGTCAGGATCCTTGTGAGGATATTTCTCGTATCCAGAA 611
 QY 590 PheGluGluLeuGlnLeuLeuGlyGlyAlaPheGlyAlaValIleValGlnAsn 609
 Db 612 TTGGAAGACTTCCCATCTTGAAGAGAGATTCGTCAGGATCCTTGTGAGGATATTTCTCGTATCCAGAA 671
 QY 610 LysLeuAspGlyCysCysTyrAlaValIleValGlyGlyAlaPheGlyAlaValIleValGlnAsn 629
 Db 672 AAATTAGATGTCAGTATTATGCAATATAAATAAATCTGATTAAAGGTGCAACTTAAACA 731
 QY 630 Phe---ArgArgIleLysGlyGluValThrLeuLeuSerArgLeuHisGlyGlnAsn 648
 Db 732 GTTTCATGAAGTCTTACGGAAGTGAAGTCTGTCAGGATCTTCACCACTCCCAATATT 791
 QY 649 ValArgTyrAsnAlaTyrPheGluArgHisGluArgProAlaGlyProGlyThrPro 668
 Db 792 GTTTCATGAAGTCTTACGGAAGTGAAGTCTGTCAGGATCTTCACCACTCCCAATATT 839
 QY 669 ProProAspSerGlyProLeuAlaLysAspAlaAlaArgGlyGlnProAla--- 687
 Db 840 -----CGAGACAGAGCTGCCATTCAGTTGCCATCTCTG 872
 QY 688 -----SerAspThrAsp 691
 Db 873 GAAGTCTCTCCGACAGAGAGAGAGAGAGATTCGTCAGGATCTTAAATAATGATGAAGT 932
 QY 692 GlyLeuAspSerValGluAlaAlaProProIleLeuSerSerVal---Glu 710
 Db 933 AGCAGCTCATCTATCTTTCTGAGCCACCCAGAGAGAGAGAGAGATTCGTCAGGATCTTAAATAATGATGAAGT 992
 QY 711 TrpSerThrSerGlyGluArgSerAlaSerAlaArgPheProAla-----ThrGlyPro 728
 Db 993 TCTGACACTGAAATCAGATTAACAAGTCGTCAGGATCTTAAATAATGATGAAGT 1052
 QY 729 GlySerSerAspGluAspAspGluAspGluHisGlyGlyValPheSerGlnSer 748
 Db 1053 GAATCTGGTGAATCTGAGTCGACCCCTGAGAGCTCCAGAGAGAGAGAGATTCGTCAGGATCTTAAATAATGATGAAGT 1112
 QY 749 PheLeuProAlaSerAspSerGluSerAspIlePheAspAsnGluAspGluAsnSer 768
 Db 1113 -----GCCAGTTCATTTGTGACAGAGAGAGAGATTCGTCAGGATCTTAAATAATGATGAAGT 1166

QY 769 LysSerGlnAsnGlnAspGluAspCysAsnGluLysAsnGlyCysHisGluSerGluPro 788
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 QY 789 SerValThrThrGluAlaValHisTyr-----LeuTyrIleGlnMetGluTyrCysGlu 806
 Db 1224 -----ACAGAGGACACATGATCCACTGATGTCACATCCAGATCCAGTGTGTGAG 1274
 QY 807 LysSerThrLeu-----ArgAspThrIleAspGln 816
 Db 1275 CTCTCCTCTGGGATTTGGATAGTCGAGAGAGAGAGAGAGAGAGAGAGATTTGGGAGAG 1334
 QY 817 GlyLeu-----TyrArgAspThrValArgLeuTyrPheArgLeuPheArgGluIleLeuAsp 834
 Db 1335 TCTGCTCTGCTCTTATGTTATGTCCTAATGTCACAAATAATTTTCAAGAAATTTGGTGA 1394
 QY 835 GlyLeuAlaTyrIleHisGluLysGlyMetIleHisArgAspLeuLysProValAsnIle 854
 Db 1395 GGTGTGTTTACATACATACATGGAATTTGTCACCCGAGATCTGAGCCCAAGAAATATT 1454
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 Db 1455 TTTCTTCTGCTGCTGATCAGCAAGTAAATAATAGGAGACTTTGGTCTGCTGCTGACAGAC 1514
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 Db 1515 ATCTCTA-----CAGAAGAGACACAGATCTGGACCAACAGAGAGAGAGAGAGAG 1559
 QY 893 AspProSerGlyHisLeuThrGlyMetValGlyThrAlaLeuTyrValSerProGlu--- 911
 Db 1560 ACACCAACA---CAT---ACGTCCAGAGTGGGTACTTGTCTGTACCTTACCCCGAACAG 1613
 QY 912 ValGlnGlySerThrLysSerAlaTyrAsnGlnLysValAspLeuPheSerLeuGlyIle 931
 Db 1614 TTGGAAGGA-----TCTGAGTATGATCCCAAGTCAGATGATGATGATGATGATGATG 1664
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 Db 1665 GTCTCTGCTGAGTCT---TTTCAGCGCTTTGGACAGAGAAATGGAGCGAGAGAGTCTTA 1721
 QY 952 AsnGlnLeuArgAspProThrSerProLysPheProGluAspPheAspAspGlyGluHis 971
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 QY 972 AlalysGlnLysSerValIleSerTrpLeuLeuAsnHisAspProAlaLysArgProThr 991
 Db 1770 CCGGTGCAAGCCAGATATATCCAGCACTTAAAGAGAGAGAGAGAGAGAGAGAGAGATCT 1829
 QY 992 AlaThrGluLeuLysSerGluLeu 1000
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 RESULT 15
 US-10-197-666A-107
 ; Sequence 107, Application US/10197666A
 ; Publication No. US2003009203A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ASAHI KASEI KANUSIKI KAISYA
 ; TITLE OF INVENTION: Elx1 phosphorylation related gene
 ; FILE REFERENCE: PH-1548US
 ; CURRENT APPLICATION NUMBER: US/10/197,666A
 ; PRIOR FILING DATE: 2002-11-18
 ; PRIOR APPLICATION NUMBER: JP 2001-218204
 ; PRIOR FILING DATE: 2001-07-18
 ; PRIOR APPLICATION NUMBER: JP 2001-263450
 ; PRIOR FILING DATE: 2001-08-31
 ; PRIOR APPLICATION NUMBER: JP 2002-012176
 ; PRIOR FILING DATE: 2002-01-21
 ; PRIOR APPLICATION NUMBER: US 60/305,884
 ; PRIOR FILING DATE: 2001-07-18
 ; PRIOR APPLICATION NUMBER: US 60/316,304
 ; PRIOR FILING DATE: 2001-09-04

; PRIOR APPLICATION NUMBER: US 60/350,027
 ; PRIOR FILING DATE: 2002-01-23
 ; NUMBER OF SEQ ID NOS: 156
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 107
 ; LENGTH: 2768
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (213)..(2069)
 ; US-10-197-666A-107

Alignment Scores:
 Pred. No.: 1,17e-35 Length: 2768
 Score: 466.50
 Percent Similarity: 44.97%
 Best Local Similarity: 30.20%
 Query Match: 5.46%
 DB: Indels: 99
 Gaps: 27

US-09-515-806A-2 (1-1649) x US-10-197-666A-107 (1-2768)

QY 472 ProTyrIysThrGlyLysLysGlyAspValTTPArgLeuGlyLeuLeuLeuSerLeu 491
 DB 370 CCCTACAGCAGCCACGCTCCCTTCCTGCTGCGAACCAG-CTGCTGCTGCTCTCTTA 428
 QY 492 SerGlnGlyGlnGluCysGlyGluTyrProValThrIleProSerAspLeuProAlaAsp 511
 DB 429 CTGGAACACTTGAGCCCATGTGCAGGCGCAACCCGCTCCACTCCAAACAGGTGTTAAA 488
 QY 512 Phe-----GlnAspPheLeuLys-----LysCysValCysLeuAspAsp 524
 DB 489 TTACTGTGCGACACTTTTATCAAGATGGGCTGCTCTCTCTTACCTGCGATGATGAG 548
 QY 525 -----LysGluArgTyrSerProGlnGlnLeuLeuLysHisSerPheIleAsnProGln 542
 DB 549 TTTACTCTCTGAGACTCCACCAACAGAGCCATCACTCATTTAATGAGGTCTGCCAAA 608
 QY 543 ProLysMetProLeuValGluGlnSerPro---GluAspSerGlyGlyGlnAspTyrVal 561
 DB 609 GAGAGA-----GTCCGTGAGATCCTTGTCAAGATAAT-----TCTTACATG 650
 QY 562 GluThrValIleProSerAsnArgLeuProSerAlaAlaPhePheSerGluThrGlnArg 581
 DB 651 CAGAAATC-----AGATCCAGAGAGATAGCCTTCGAACGCAAAACG----- 692
 QY 582 GlnPheSerArgTyrPheIleGluPheGluGluGlnLeuLeuGlyLysGlyAlaPhe 601
 DB 693 -----TCACGCTACTTAATGAATTTGAAGAGCTTGCCATATGCAATTAAGAAATC 746
 QY 602 GlyAlaValIleLysValGlnAsnLysLeuAspGlyCysCysTyrAlaValLysArgile 621
 DB 747 GGAAGAGTTTACAGGTCCGGAACAAATTAGATGGTCACCATATGCAATTAAGAAATC 806
 QY 622 ProIleAsnProAlaSerArg---GlnPheArgArgileLysGlyGluValThrLeu 640
 DB 807 CTGATTAAAGAGCGCACTAAACAGAGATTGTATGAAGGTGCTACGGGAAGTGAAGTCTG 866
 QY 641 SerArgLeuHisGluAsnIleValArgTyrTyrAsnAlaTTPileGluArg---His 659
 DB 867 GCAGGTCTCCAGCATCCCAATATTTGGCTACACACTGCTGGTGAATGAACATGTTTCAT 926
 QY 660 GluArgProAlaGlyProGlyThrProProAspSerGlyProLeuAlaLysAspAsp 679
 DB 927 GTG-----GTTCCAGCCCAACAGACAGAGTTCGGAATTCACCTGCCCTCT 968
 QY 680 ArgAlaAlaArgGlyGlnProAlaSerAspThrAsp-----GlyLeuAspSerValGlu 697
 DB 969 CTCGAAGTCTCTCGGAGCAGGAGGGGACAGACCAAGGTGTGTTAAGATAATGAA 1028
 QY 698 AlaAlaAla-----ProProIleLeuSer 706

DB 1029 AGCATTGCTCCATTGCTTGTGCTGAACCTACCCCAAGAAAGAAACCTTTTGGGAG 1088
 QY 707 SerSerValGluThrPsrThrSerGlyGluArgSerAlaSerAlaArgPheProAlaThr 726
 DB 1089 TCTGAGGTTAAAAATGAGATAACAACCTGGTGTACCGGCCAACCTTAGTGTGTCAG 1148
 QY 727 GlyProGlySerSerAspGluAspAspGluAspGluHisGlyGlyValPheSer 746
 DB 1149 -----AACAGCAGTGAAGTGAATCGTCCATTGAGCTCCAAGAGACGCTTGACTGAT 1202
 QY 747 GlnSerPheLeuProAlaSerAspSerGluSerAspIleIlePheAspAsnGluAspGlu 766
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 QY 767 AsnSerLysSerGlnAsnGlnAspGluAspCysAsnGluLysAsnGlyCysHisGluSer 786
 DB 1263 GGGAAATTTACATCCACGATCAGTCTTCTGAAGCAACTTGAACCTCTGCGGCAGACG 1322
 QY 787 GluProSerValThrGluAlaValHisTyr-----LeuTyrIleGlnMetGlu 803
 DB 1323 GAC-----GTTCCGTACCACTGATGTTGCCACATCCAGATCGAG 1361
 QY 804 TyrCysGluLysSer-----ThrLeuArgAspThr 813
 DB 1362 CTGTGTGAGCTCTCCCTCTGGGACTGGATAACTCAGAGGAACAACGCGGAGTAT 1421
 QY 814 IleAspGlnGlyLeu-----TyrArgAspThrValArgLeuTyrArgLeuPheArgGlu 831
 DB 1422 GTGGAGCAAGCTGCTGCTCCCTATGTTATGGCCAGTGTTCACAAACAAATTTTCAAGAA 1481
 QY 832 IleLeuAspGlyLeuAlaTyrIleHisGluLysGlyMetIleHisArgAspLeuLysPro 851
 DB 1482 TTGGTGAAGGTGCTTTTATACATAAATGCGCATGTCACAGAGATCTGAAGCCT 1541
 QY 852 ValAsnIlePheLeuAspSer---AspAspHisValLysIleGlyAspPheGlyLeuAla 870
 DB 1542 AGAAATATTTTCTTCATGCGCCCTGATCAGCAAGTAAATAATAGGAGACTTGTCTGCGCC 1601
 QY 871 ThrAspHisLeuAlaPheSerAlaAspSerLysGlnAspAspGlnThrGlyAspLeuIle 890
 DB 1602 -----TGTCAGACATCATCCAGATG--CAGACTGACCAACAGAA 1641
 QY 891 LysSerAspProSerGlyHisLeuThrGlyMetValGlyThrAlaLeuTyrValSerPro 910
 DB 1642 ATGGGAAGGAACACCGACACAC-ACATCCAGAGTGGGACTTGTCTACGCATCACCG 1700
 QY 911 Glu---ValGlnGlySerThrLysSerAlaTyrAsnGlnLysValAspLeuPheSerLeu 929
 DB 1701 GAACAGCTGGAGGA-----TCCAGATAGATGCCAAGTCAGATATGTATAGCTTG 1751
 QY 930 GlyIleIlePhePheGluMetSerTyrHisProMetValThrAlaSerGluArgilePhe 949
 DB 1752 GGTGTGATCTCTCGAGCTC---TTTCAGCCATTCGGGACAGAAATGGAGGGGCAACA 1808
 QY 950 ValLeuAsnGlnLeuArgAspProThrSerProLysPheProGluAspPheAspAspGly 969
 DB 1809 GTCTTAACAGGCGTAAGG-----ACTGTCGGATACCCGAATCCCTCAGTAA-- 1856
 QY 970 GluHisAlaLysGlnLysSerValIleSerTrpLeuLeuAsnHisAspProAlaLysArg 989
 DB 1857 AGGTCTCGGTGCAAGCCCAAGTATATCCAGCTCTAACCGGAGGAATGTGTACAGAGA 1916
 QY 990 ProThrAlaThrGluLeuLysSerGluLeuLeuProPro----- 1004
 DB 1917 CCATGCGCTTCAGCTGCTGCAGAGTGAGCTTTTCAACAACTGGAATGTTAATCTC 1976
 QY 1005 -----GlnMet-----GluGluSerGluLeuHisGluVal 1014
 DB 1977 ACATTGCAGATGAAGATAATAGAACCAAGAGAGAAATTAAGAACTA 2024

Search completed: June 12, 2003, 08:25:30
 Job time : 1084 secs

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